

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Metz, James G.
Lardizabal, Kathryn D.
Lassner, Michael

(ii) TITLE OF INVENTION: Nucleic Acid Sequences Encoding in A
Cytoplasmic Protein Involved in Fatty Acyl-CoA Metabolism

(iii) NUMBER OF SEQUENCES: 39

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Davis

(D) STATE: CA

(E) COUNTRY: USA

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB

(B) COMPUTER: Apple Macintosh

(C) OPERATING SYSTEM: Macintosh 7.0

(D) SOFTWARE: Microsoft Word 5.1a

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/657,749

(B) FILING DATE: 30-MAY-96

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US94/13686

(B) FILING DATE: 30-NOV-94

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/265,047

(B) FILING DATE: 23-JUN-94

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/160,602

(B) FILING DATE: 30-NOV-93

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/066,299

(B) FILING DATE: 20-MAY-93

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US92/09863

(B) FILING DATE: 13-NOV-92

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/933,411

(B) FILING DATE: 21-AUG-92

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/796,256

(B) FILING DATE: 20-NOV-91

(viii) ATTORNEY/AGENT INFORMATION:

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1786 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
AAATCCTCCA CTCATACACT CCACTTCTCT CTCTCTCTCT CTCTCTCTGA AACAAATTTGA      60

GTAGCAAACCT TAAAAGAAA ATG GAG GAA ATG GGA AGC ATT TTA GAG TTT CTT      112
                Met Glu Glu Met Gly Ser Ile Leu Glu Phe Leu
                1                5                10

GAT AAC AAA GCC ATT TTG GTC ACT GGT GCT ACT GGC TCC TTA GCA AAA      160
Asp Asn Lys  Ala Ile Leu Val Thr Gly Ala Thr Gly Ser  Leu Ala Lys
                15                20                25

ATT TTT GTG GAG AAG GTA CTG AGG AGT CAA CCG AAT GTG AAG AAA CTC      208
Ile Phe Val Glu Lys Val Leu Arg Ser Gln Pro Asn Val Lys Lys Leu
                30                35                40

TAT CTT CTT TTG AGA GCA ACC GAT GAC GAG ACA GCT GCT CTA CGC TTG      256
Tyr Leu Leu Leu Arg Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu
                45                50                55

CAA AAT GAG GTT TTT GGA AAA GAG TTG TTC AAA GTT CTG AAA CAA AAT      304
Gln Asn Glu Val Phe Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn
        60                65                70                75

TTA GGT GCA AAT TTC TAT TCC TTT GTA TCA GAA AAA GTG ACT GTA GTA      352
Leu Gly Ala Asn Phe Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val
                80                85                90
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CCC	GGT	GAT	ATT	ACT	GGT	GAA	GAC	TTG	TGT	CTC	AAA	GAC	GTC	AAT	TTG	400
Pro	Gly	Asp	Ile	Thr	Gly	Glu	Asp	Leu	Cys	Leu	Lys	Asp	Val	Asn	Leu	
			95					100					105			
AAG	GAA	GAA	ATG	TGG	AGG	GAA	ATC	GAT	GTT	GTT	GTC	AAT	CTA	GCT	GCT	448
Lys	Glu	Glu	Met	Trp	Arg	Glu	Ile	Asp	Val	Val	Val	Asn	Leu	Ala	Ala	
		110					115					120				
ACA	ATC	AAC	TTC	ATT	GAA	AGG	TAC	GAC	GTG	TCT	CTG	CTT	ATC	AAC	ACA	496
Thr	Ile	Asn	Phe	Ile	Glu	Arg	Tyr	Asp	Val	Ser	Leu	Leu	Ile	Asn	Thr	
	125					130					135					
TAT	GGA	GCC	AAG	TAT	GTT	TTG	GAC	TTC	GCG	AAG	AAG	TGC	AAC	AAA	TTA	544
Tyr	Gly	Ala	Lys	Tyr	Val	Leu	Asp	Phe	Ala	Lys	Lys	Cys	Asn	Lys	Leu	
140					145					150					155	
AAG	ATA	TTT	GTT	CAT	GTA	TCT	ACT	GCT	TAT	GTA	TCT	GGA	GAG	AAA	AAT	592
Lys	Ile	Phe	Val	His	Val	Ser	Thr	Ala	Tyr	Val	Ser	Gly	Glu	Lys	Asn	
				160					165					170		
GGG	TTA	ATA	CTG	GAG	AAG	CCT	TAT	TAT	ATG	GGC	GAG	TCA	CTT	AAT	GGA	640
Gly	Leu	Ile	Leu	Glu	Lys	Pro	Tyr	Tyr	Met	Gly	Glu	Ser	Leu	Asn	Gly	
			175					180					185			
AGA	TTA	GGT	CTG	GAC	ATT	AAT	GTA	GAG	AAG	AAA	CTT	GTG	GAG	GCA	AAA	688
Arg	Leu	Gly	Leu	Asp	Ile	Asn	Val	Glu	Lys	Lys	Leu	Val	Glu	Ala	Lys	
		190					195					200				
ATC	AAT	GAA	CTT	CAA	GCA	GCG	GGG	GCA	ACG	GAA	AAG	TCC	ATT	AAA	TCG	736
Ile	Asn	Glu	Leu	Gln	Ala	Ala	Gly	Ala	Thr	Glu	Lys	Ser	Ile	Lys	Ser	
	205					210					215					
ACA	ATG	AAG	GAC	ATG	GGC	ATC	GAG	AGG	GCA	AGA	CAC	TGG	GGA	TGG	CCA	784
Thr	Met	Lys	Asp	Met	Gly	Ile	Glu	Arg	Ala	Arg	His	Trp	Gly	Trp	Pro	
220					225					230					235	
AAT	GTG	TAT	GTA	TTC	ACC	AAG	GCA	TTA	GGG	GAG	ATG	CTT	TTG	ATG	CAA	832
Asn	Val	Tyr	Val	Phe	Thr	Lys	Ala	Leu	Gly	Glu	Met	Leu	Leu	Met	Gln	
				240					245					250		
TAC	AAA	GGG	GAC	ATT	CCG	CTT	ACT	ATT	ATT	CGT	CCC	ACC	ATC	ATC	ACC	880
Tyr	Lys	Gly	Asp	Ile	Pro	Leu	Thr	Ile	Ile	Arg	Pro	Thr	Ile	Ile	Thr	
			255					260					265			

AGC	ACT	TTT	AAA	GAG	CCC	TTT	CCT	GGT	TGG	GTT	GAA	GGT	GTC	AGG	ACC	928
Ser	Thr	Phe	Lys	Glu	Pro	Phe	Pro	Gly	Trp	Val	Glu	Gly	Val	Arg	Thr	
		270					275					280				
ATC	GAT	AAT	GTA	CCT	GTA	TAT	TAT	GGT	AAA	GGG	AGA	TTG	AGG	TGT	ATG	976
Ile	Asp	Asn	Val	Pro	Val	Tyr	Tyr	Gly	Lys	Gly	Arg	Leu	Arg	Cys	Met	
	285					290					295					
CTT	TGC	GGA	CCC	AGC	ACA	ATA	ATT	GAC	CTG	ATA	CCG	GCA	GAT	ATG	GTC	1024
Leu	Cys	Gly	Pro	Ser	Thr	Ile	Ile	Asp	Leu	Ile	Pro	Ala	Asp	Met	Val	
300					305					310					315	
GTG	AAT	GCA	ACG	ATA	GTA	GCC	ATG	GTG	GCG	CAC	GCA	AAC	CAA	AGA	TAC	1072
Val	Asn	Ala	Thr	Ile	Val	Ala	Met	Val	Ala	His	Ala	Asn	Gln	Arg	Tyr	
				320					325					330		
GTA	GAG	CCG	GTG	ACA	TAC	CAT	GTG	GGA	TCT	TCA	GCG	GCG	AAT	CCA	ATG	1120
Val	Glu	Pro	Val	Thr	Tyr	His	Val	Gly	Ser	Ser	Ala	Ala	Asn	Pro	Met	
			335					340					345			
AAA	CTG	AGT	GCA	TTA	CCA	GAG	ATG	GCA	CAC	CGT	TAC	TTC	ACC	AAG	AAT	1168
Lys	Leu	Ser	Ala	Leu	Pro	Glu	Met	Ala	His	Arg	Tyr	Phe	Thr	Lys	Asn	
		350					355					360				
CCA	TGG	ATC	AAC	CCG	GAT	CGC	AAC	CCA	GTA	CAT	GTG	GGT	CGG	GCT	ATG	1216
Pro	Trp	Ile	Asn	Pro	Asp	Arg	Asn	Pro	Val	His	Val	Gly	Arg	Ala	Met	
	365					370					375					
GTC	TTC	TCC	TCC	TTC	TCC	ACC	TTC	CAC	CTT	TAT	CTC	ACC	CTT	AAT	TTC	1264
Val	Phe	Ser	Ser	Phe	Ser	Thr	Phe	His	Leu	Tyr	Leu	Thr	Leu	Asn	Phe	
380					385				390						395	
CTC	CTT	CCT	TTG	AAG	GTA	CTG	GAG	ATA	GCA	AAT	ACA	ATA	TTC	TGC	CAA	1312
Leu	Leu	Pro	Leu	Lys	Val	Leu	Glu	Ile	Ala	Asn	Thr	Ile	Phe	Cys	Gln	
				400					405					410		
TGG	TTC	AAG	GGT	AAG	TAC	ATG	GAT	CTT	AAA	AGG	AAG	ACG	AGG	TTG	TTG	1360
Trp	Phe	Lys	Gly	Lys	Tyr	Met	Asp	Leu	Lys	Arg	Lys	Thr	Arg	Leu	Leu	
			415					420					425			
TTG	CGT	TTA	GTA	GAC	ATT	TAT	AAA	CCC	TAC	CTC	TTC	TTC	CAA	GGC	ATC	1408
Leu	Arg	Leu	Val	Asp	Ile	Tyr	Lys	Pro	Tyr	Leu	Phe	Phe	Gln	Gly	Ile	
		430					435					440				

TTT GAT GAC ATG AAC ACT GAG AAG TTG CGG ATT GCT GCA AAA GAA AGC 1456
Phe Asp Asp Met Asn Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser
445 450 455

ATA GTT GAA GCT GAT ATG TTT TAC TTT GAT CCC AGG GCA ATT AAC TGG 1504
Ile Val Glu Ala Asp Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp
460 465 470 475

GAA GAT TAC TTC TTG AAA ACT CAT TTC CCA GGN GTC GTA GAG CAC GTT 1552
Glu Asp Tyr Phe Leu Lys Thr His Phe Pro Gly Val Val Glu His Val
480 485 490

CTT AAC TAAAAGTTAC GGTACGAAAA TGAGAAGATT GGAATGCATG CACCGAAAGN 1608
Leu Asn

NCAACATAAA AGACGTGGTT AAAGTCATGG TCAAAAAAGA AATAAAATGC AGTTAGGTTT 1668

GTGTTGCAGT TTTGATTCCCT TGTATTGTTA CTTGTACTTT TGATCTTTTT CTTTTTTAAT 1728

GAAATTTCTC TCTTTGTTTT GTGAAAAAAA AAAAAAAAAA GAGCTCCTGC AGAAGCTT 1786

(2) INFORMATION FOR SEQ ID NO: 2 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1733 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2 :

GGAACTCCAT CCCTTCCTCC CTCCTCCTC TCTCTACA ATG AAG GCC AAA ACA ATC 56
Met Lys Ala Lys Thr Ile
1 5

ACA AAC CCG GAG ATC CAA GTC TCC ACG ACC ATG ACC ACC ACG ACC ACG 104
Thr Asn Pro Glu Ile Gln Val Ser Thr Thr Met Thr Thr Thr Thr Thr
10 15 20

ACT	ATG	ACC	GCC	ACT	CTC	CCC	AAC	TTC	AAG	TCC	TCC	ATC	AAC	TTA	CAC	152
Thr	Met	Thr	Ala	Thr	Leu	Pro	Asn	Phe	Lys	Ser	Ser	Ile	Asn	Leu	His	
		25					30					35				
CAC	GTC	AAG	CTC	GGC	TAC	CAC	TAC	TTA	ATC	TCC	AAT	GCC	CTC	TTC	CTC	200
His	Val	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	Ser	Asn	Ala	Leu	Phe	Leu	
	40					45					50					
GTA	TTC	ATC	CCC	CTT	TTG	GGC	CTC	GCT	TCG	GCC	CAT	CTC	TCC	TCC	TTC	248
Val	Phe	Ile	Pro	Leu	Leu	Gly	Leu	Ala	Ser	Ala	His	Leu	Ser	Ser	Phe	
55					60					65					70	
TCG	GCC	CAT	GAC	TTG	TCC	CTG	CTC	TTC	GAC	CTC	CTT	CGC	CGC	AAC	CTC	296
Ser	Ala	His	Asp	Leu	Ser	Leu	Leu	Phe	Asp	Leu	Leu	Arg	Arg	Asn	Leu	
			75						80					85		
CTC	CCT	GTT	GTC	GTT	TGT	TCT	TTC	CTC	TTC	GTT	TTA	TTA	GCA	ACC	CTA	344
Leu	Pro	Val	Val	Val	Cys	Ser	Phe	Leu	Phe	Val	Leu	Leu	Ala	Thr	Leu	
			90					95					100			
CAT	TTC	TTG	ACC	CGG	CCC	AGG	AAT	GTC	TAC	TTG	GTG	GAC	TTT	GGA	TGC	392
His	Phe	Leu	Thr	Arg	Pro	Arg	Asn	Val	Tyr	Leu	Val	Asp	Phe	Gly	Cys	
		105					110					115				
TAT	AAG	CCT	CAA	CCG	AAC	CTG	ATG	ACA	TCC	CAC	GAG	ATG	TTC	ATG	GAC	440
Tyr	Lys	Pro	Gln	Pro	Asn	Leu	Met	Thr	Ser	His	Glu	Met	Phe	Met	Asp	
	120					125					130					
CGG	ACC	TCC	CGG	GCC	GGG	TCG	TTT	TCT	AAG	GAG	AAT	ATT	GAG	TTT	CAG	488
Arg	Thr	Ser	Arg	Ala	Gly	Ser	Phe	Ser	Lys	Glu	Asn	Ile	Glu	Phe	Gln	
135					140					145					150	
AGG	AAG	ATC	TTG	GAG	AGG	GCC	GGT	ATG	GGT	CGG	GAA	ACC	TAT	GTC	CCC	536
Arg	Lys	Ile	Leu	Glu	Arg	Ala	Gly	Met	Gly	Arg	Glu	Thr	Tyr	Val	Pro	
				155					160					165		
GAA	TCC	GTC	ACT	AAG	GTG	CCC	GCC	GAG	CCG	AGC	ATA	GCA	GCA	GCC	AGG	584
Glu	Ser	Val	Thr	Lys	Val	Pro	Ala	Glu	Pro	Ser	Ile	Ala	Ala	Ala	Arg	
			170					175					180			

GCC Ala	GAG Glu	GCG Ala	GAG Glu	GAG Glu	GTG Val	ATG Met	TAC Tyr	GGG Gly	GCG Ala	ATC Ile	GAC Asp	GAG Glu	GTG Val	TTG Leu	GAG Glu	632
		185					190					195				
AAG Lys	ACG Thr	GGG Gly	GTG Val	AAG Lys	CCG Pro	AAG Lys	CAG Gln	ATA Ile	GGA Gly	ATA Ile	CTG Leu	GTG Val	GTG Val	ANC Xxx	TGC Cys	680
	200					205					210					
AGC Ser	TTG Leu	TTT Phe	AAC Asn	CCA Pro	ACG Thr	CCG Pro	TCG Ser	CTG Leu	TCA Ser	TCC Ser	ATG Met	ATA Ile	GTT Val	AAC Asn	CAT His	728
215					220					225					230	
TAC Tyr	AAG Lys	CTN Leu	AGG Arg	GGT Gly	AAT Asn	ATA Ile	CTT Leu	AGC Ser	TAT Tyr	AAT Asn	CTT Leu	GGT Gly	GGC Gly	ATG Met	GGT Gly	776
				235					240					245		
TGC Cys	AGT Ser	GCT Ala	GGG Gly	CTC Leu	ATT Ile	TCC Ser	ATT Ile	GAT Asp	CTT Leu	GCC Ala	AAG Lys	GAC Asp	CTC Leu	CTA Leu	CAG Gln	824
			250					255					260			
GTT Val	TAC Tyr	CGT Arg	AAA Lys	AAC Asn	ACA Thr	TAT Tyr	GTG Val	TTA Leu	GTA Val	GTG Val	AGC Ser	ACG Thr	GAA Glu	AAC Asn	ATG Met	872
		265					270					275				
ACC Thr	CTT Leu	AAT Asn	TGG Trp	TAC Tyr	TGG Trp	GGC Gly	AAT Asn	GAC Asp	CGC Arg	TCC Ser	ATG Met	CTT Leu	ATC Ile	ACC Thr	AAC Asn	920
	280					285					290					
TGC Cys	CTA Leu	TTT Phe	CGC Arg	ATG Met	GGT Gly	GGC Gly	GCT Ala	GCC Ala	ATC Ile	ATC Ile	CTC Leu	TCA Ser	AAC Asn	CGC Arg	TGG Trp	968
295					300					305					310	
CGT Arg	GAT Asp	CGT Arg	CGC Arg	CGA Arg	TCC Ser	AAG Lys	TAC Tyr	CAA Gln	CTC Leu	CTT Leu	CAT His	ACA Thr	GTA Val	CGC Arg	ACC Thr	1016
				315					320					325		
CAC His	AAG Lys	GGC Gly	GCT Ala	GAC Asp	GAC Asp	AAG Lys	TCC Ser	TAT Tyr	AGA Arg	TGC Cys	GTC Val	TTA Leu	CAA Gln	CAA Gln	GAA Glu	1064
			330					335					340			
GAT Asp	GAA Glu	AAT Asn	AAC Asn	AAG Lys	GTA Val	GGT Gly	GTT Val	GCC Ala	TTA Leu	TCC Ser	AAG Lys	GAT Asp	CTG Leu	ATG Met	GCA Ala	1112
		345					350					355				

GTT	GCC	GGT	GAA	GCC	CTA	AAG	GCC	AAC	ATC	ACG	ACC	CTT	GGT	CCC	CTC	1160
Val	Ala	Gly	Glu	Ala	Leu	Lys	Ala	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	
	360					365					370					
GTG	CTC	CCC	ATG	TCA	GAA	CAA	CTC	CTC	TTC	TTT	GCC	ACC	TTA	GTG	GCA	1208
Val	Leu	Pro	Met	Ser	Glu	Gln	Leu	Leu	Phe	Phe	Ala	Thr	Leu	Val	Ala	
	375				380					385					390	
CGT	AAG	GTC	TTC	AAG	ATG	ACG	AAC	GTG	AAG	CCA	TAC	ATC	CCA	GAT	TTC	1256
Arg	Lys	Val	Phe	Lys	Met	Thr	Asn	Val	Lys	Pro	Tyr	Ile	Pro	Asp	Phe	
				395					400					405		
AAG	TTG	GCA	GCG	AAC	GAC	TTC	TGC	ATC	CAT	GCA	GGA	GGC	AAA	GCA	GTG	1304
Lys	Leu	Ala	Ala	Asn	Asp	Phe	Cys	Ile	His	Ala	Gly	Gly	Lys	Ala	Val	
			410					415					420			
TTG	GAT	GAG	CTC	GAG	AAG	AAC	TTG	GAG	TTG	ACG	CCA	TGG	CAC	CTT	GAA	1352
Leu	Asp	Glu	Leu	Glu	Lys	Asn	Leu	Glu	Leu	Thr	Pro	Trp	His	Leu	Glu	
		425					430					435				
CCC	TCG	AGG	ATG	ACA	CTG	TAT	AGG	TTT	GGG	AAC	ACA	TCG	AGT	AGC	TCA	1400
Pro	Ser	Arg	Met	Thr	Leu	Tyr	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	
	440					445					450					
TTA	TGG	TAC	GAG	TTG	GCA	TAC	GCT	GAA	GCA	AAA	GGG	AGG	ATC	CGT	AAG	1448
Leu	Trp	Tyr	Glu	Leu	Ala	Tyr	Ala	Glu	Ala	Lys	Gly	Arg	Ile	Arg	Lys	
	455				460					465					470	
GGT	GAT	CGA	ACT	TGG	ATG	ATT	GGA	TTT	GGT	TCA	GGT	TTC	AAG	TGT	AAC	1496
Gly	Asp	Arg	Thr	Trp	Met	Ile	Gly	Phe	Gly	Ser	Gly	Phe	Lys	Cys	Asn	
				475					480					485		
AGT	GTT	GTG	TGG	AGG	GCT	TTG	AGG	AGT	GTC	AAT	CCG	GCT	AGA	GAG	AAG	1544
Ser	Val	Val	Trp	Arg	Ala	Leu	Arg	Ser	Val	Asn	Pro	Ala	Arg	Glu	Lys	
			490					495					500			
AAT	CCT	TGG	ATG	GAT	GAA	ATT	GAG	AAG	TTC	CCT	GTC	CAT	GTG	CCT	AAA	1592
Asn	Pro	Trp	Met	Asp	Glu	Ile	Glu	Lys	Phe	Pro	Val	His	Val	Pro	Lys	
		505					510					515				

ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT TAGTAATGAA 1640
 Ile Ala Pro Ile Ala Ser
 520

AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT GAGAACATGT 1700
 CTCATTGAGA ATAACGTGTG CATCGTTGTG TTG 1733

(2) INFORMATION FOR SEQ ID NO:3 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3 :

GTCGACACA ATG AAG GCC AAA ACA ATC ACA AAC CCG GAG ATC CAA GTC TCC 51
 Met Lys Ala Lys Thr Ile Thr Asn Pro Glu Ile Gln Val Ser
 1 5 10

ACG ACC ATG ACC ACC ACG ACC ACG ACC GCC ACT CTC CCC AAC TTC AAG 99
 Thr Thr Met Thr Thr Thr Thr Thr Ala Thr Leu Pro Asn Phe Lys
 15 20 25 30

TCC TCC ATC AAC TTA CAC CAC GTC AAG CTC GGC TAC CAC TAC TTA ATC 147
 Ser Ser Ile Asn Leu His His Val Lys Leu Gly Tyr His Tyr Leu Ile
 35 40 45

TCC AAT GCC CTC TTC CTC GTA TTC ATC CCC CTT TTG GGC CTC GCT TCG 195
 Ser Asn Ala Leu Phe Leu Val Phe Ile Pro Leu Leu Gly Leu Ala Ser
 50 55 60

GCC CAC CTC TCC TCC TTC TCG GCC CAT GAC TTG TCC CTG CTC TTC GAC 243
 Ala His Leu Ser Ser Phe Ser Ala His Asp Leu Ser Leu Leu Phe Asp
 65 70 75

CTC	CTT	CGC	CGC	AAC	CTC	CTC	CCC	GTT	GTC	GTT	TGT	TCT	TTC	CTC	TTC	291
Leu	Leu	Arg	Arg	Asn	Leu	Leu	Pro	Val	Val	Val	Cys	Ser	Phe	Leu	Phe	
80						85					90					
GTT	TTA	TTA	GCA	ACC	CTA	CAT	TTC	TTG	ACC	CGG	CCT	AGG	AAT	GTC	TAC	339
Val	Leu	Leu	Ala	Thr	Leu	His	Phe	Leu	Thr	Arg	Pro	Arg	Asn	Val	Tyr	
95					100					105					110	
TTG	GTG	GAC	TTT	GCC	TGC	TAT	AAG	CCT	CAC	CCG	AAC	CTG	ATA	ACA	TCC	387
Leu	Val	Asp	Phe	Ala	Cys	Tyr	Lys	Pro	His	Pro	Asn	Leu	Ile	Thr	Ser	
				115					120					125		
CAC	GAG	ATG	TTC	ATG	GAC	CGG	ACC	TCC	CGG	GCC	GGG	TCG	TTT	TCT	AAG	435
His	Glu	Met	Phe	Met	Asp	Arg	Thr	Ser	Arg	Ala	Gly	Ser	Phe	Ser	Lys	
			130					135					140			
GAG	AAT	ATT	GAG	TTT	CAG	AGG	AAG	ATC	TTG	GAG	AGG	GCC	GGT	ATG	GGC	483
Glu	Asn	Ile	Glu	Phe	Gln	Arg	Lys	Ile	Leu	Glu	Arg	Ala	Gly	Met	Gly	
		145					150					155				
CGG	GAA	ACC	TAC	GTC	CCC	GAA	TCC	GTC	ACT	AAG	GTG	CCG	CCC	GAG	CCG	531
Arg	Glu	Thr	Tyr	Val	Pro	Glu	Ser	Val	Thr	Lys	Val	Pro	Pro	Glu	Pro	
	160					165					170					
AGC	ATA	GCA	GCA	GCC	AGG	GCC	GAG	GCG	GAG	GAG	GTG	ATG	TAC	GGG	GCG	579
Ser	Ile	Ala	Ala	Ala	Arg	Ala	Glu	Ala	Glu	Glu	Val	Met	Tyr	Gly	Ala	
175					180					185					190	
ATC	GAC	GAG	GTG	TTG	GAG	AAG	ACG	GGG	GTG	AAG	CCG	AAG	CAG	ATA	GGA	627
Ile	Asp	Glu	Val	Leu	Glu	Lys	Thr	Gly	Val	Lys	Pro	Lys	Gln	Ile	Gly	
				195				200						205		
ATA	CTG	GTG	GTG	AAC	TGC	AGC	TTG	TTT	AAC	CCA	ACG	CCG	TCG	CTG	TCA	675
Ile	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	
			210					215					220			
TCC	ATG	ATA	GTT	AAC	CAT	TAC	AAG	CTT	AGG	GGT	AAT	ATA	CTT	AGC	TAT	723
Ser	Met	Ile	Val	Asn	His	Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	
		225					230					235				
AAT	CTT	GGT	GGC	ATG	GGT	TGC	AGT	GCT	GGG	CTC	ATT	TCC	ATT	GAT	CTT	771
Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly	Leu	Ile	Ser	Ile	Asp	Leu	
	240					245					250					

GCC Ala 255	AAG Lys	GAC Asp	CTC Leu	CTA Leu	CAG Gln 260	GTT Val	TAC Tyr	CGT Arg	AAC Asn	ACA Thr 265	TAT Tyr	GTG Val	TTA Leu	GTA Val	GTG Val 270	819
AGC Ser	ACA Thr	GAA Glu	AAC Asn	ATG Met 275	ACC Thr	CTT Leu	AAT Asn	TGG Trp	TAC Tyr 280	TGG Trp	GGC Gly	AAT Asn	GAC Asp	CGC Arg 285	TCC Ser	867
ATG Met	CTT Leu	ATC Ile	ACC Thr 290	AAC Asn	TGC Cys	CTA Leu	TTT Phe	CGC Arg 295	ATG Met	GGT Gly	GGC Gly	GCT Ala	GCC Ala 300	ATC Ile	ATC Ile	915
CTC Leu	TCA Ser	AAC Asn 305	CGC Arg	TGG Trp	CGT Arg	GAT Asp	CGT Arg 310	CGC Arg	CGA Arg	TCC Ser	AAG Lys	TAC Tyr 315	CAA Gln	CTC Leu	CTT Leu	963
CAC His 320	ACA Thr	GTA Val	CGC Arg	ACC Thr	CAC His	AAG Lys 325	GGC Gly	GCT Ala	GAC Asp	GAC Asp	AAG Lys 330	TCC Ser	TAT Tyr	AGA Arg	TGC Cys	1011
GTC Val 335	TTA Leu	CAA Gln	CAA Gln	GAA Glu	GAT Asp 340	GAA Glu	AAT Asn	AAC Asn	AAG Lys	GTA Val 345	GGT Gly	GTT Val	GCC Ala	TTA Leu	TCC Ser 350	1059
AAG Lys	GAT Asp	CTG Leu	ATG Met	GCA Ala 355	GTT Val	GCC Ala	GGT Gly	GAA Glu	GCC Ala 360	CTA Leu	AAG Lys	GCC Ala	AAC Asn	ATC Ile 365	ACG Thr	1107
ACC Thr	CTT Leu	GGT Gly	CCC Pro 370	CTC Leu	GTG Val	CTC Leu	CCC Pro	ATG Met 375	TCA Ser	GAA Glu	CAA Gln	CTC Leu	CTC Leu	TTC Phe 380	TTT Phe	1155
GCC Ala	ACC Thr	TTA Leu 385	GTG Val	GCA Ala	CGT Arg	AAG Lys	GTC Val 390	TTC Phe	AAG Lys	ATG Met	ACG Thr	AAC Asn 395	GTG Val	AAG Lys	CCA Pro	1203
TAC Tyr 400	ATC Ile	CCA Pro	GAT Asp	TTC Phe	AAG Lys	TTG Leu 405	GCA Ala	GCG Ala	AAG Lys	CAC His	TTC Phe 410	TGC Cys	ATC Ile	CAT His	GCA Ala	1251
GGA Gly	GGC Gly	AAA Lys	GCA Ala	GTG Val	TTG Leu	GAT Asp	GAG Glu	CTC Leu	GAG Glu	ACG Thr	AAC Asn	TTG Leu	GAG Glu	TTG Leu	ACG Thr	1299

415		420		425		430	
CCA TGG CAC CTT GAA CCC TCG AGG ATG ACA CTG TAT AGG TTT GGG AAC	1347						
Pro Trp His Leu Glu Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn							
		435		440		445	
ACA TCG AGT AGC TCA TTA TGG TAC GAG TTG GCA TAC GCT GAA GCA AAA	1395						
Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys							
		450		455		460	
GGG AGG ATC CGT AAG GGT GAT CGA ACT TGG ATG ATT GGA TTT GGT TCA	1443						
Gly Arg Ile Arg Lys Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser							
		465		470		475	
GGT TTC AAG TGT AAC AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT	1491						
Gly Phe Lys Cys Asn Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn							
		480		485		490	
CCG GCT AGA GAG AAG AAT CCT TGG ATG GAT GAA ATT GAG AAT TTC CCT	1539						
Pro Ala Arg Glu Lys Asn Pro Trp Met Asp Glu Ile Glu Asn Phe Pro							
		495		500		505	
GTC CAT GTG CCT AAA ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT	1592						
Val His Val Pro Lys Ile Ala Pro Ile Ala Ser							
		515		520			
TAGTAATGAA AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAACTTTA GTTGATGGGT	1652						
GAGAACATGT CTCATTGAGA ATAACGTGTG CATCGTTGTG TTGAATTTGA ATTTGAGTAT	1712						
TGGTGAAATT CTGTTAGAAT TGACGCATGA GTCATATATA TACAAATTTA AGTAAGATTT	1772						
TACGCTTTCT T	1783						

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1647 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: PCR to genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4 :

```
GGCGCGCCGG TACCTCTAGA CCTGGCGATT CAACGTGGTC GGATCATGAC GCTTCCAGAA      60
AACATCGAGC AAGCTCTCAA AGCTGACCTC TTTCGGATCG TACTGAACCC GAACAATCTC     120
GTTATGTCCC GTCGTCTCCG AACAGACATC CTCGTAGCTC GGATTATCGA CGAATCCATG     180
GCTATACCCA ACCTCCGTCT TCGTCACGCC TGGAACCCTC TGGTACGCCA ATTCCGCTCC     240
CCAGAAGCAA CCGGCGCCGA ATTGCGCGAA TTGCTGACCT GGAGACGGAA CATCGTCGTC     300
GGGTCCTTGC GCGATTGCGG CGGAAGCCGG GTCGGGTTGG GGACGAGACC CGAATCCGAG     360
CCTGGTGAAG AGGTTGTTCA TCGGAGATTT ATAGACGGAG ATGGATCGAG CGGTTTTGGG     420
GAAAGGGGAA GTGGGTTTGG CTCTTTTGA TAGAGAGAGT GCAGCTTTGG AGAGAGACTG     480
GAGAGGTTTA GAGAGAGACG CGGCGGATAT TACCGGAGGA GAGGCGACGA GAGATAGCAT     540
TATCGAAGGG GAGGGAGAAA GAGTGACGTG GAGAAATAAG AAACCGTTAA GAGTCGGATA     600
TTTATCATAT TAAAAGCCCA ATGGGCCTGA ACCCATTTAA ACAAGACAGA TAAATGGGCC     660
GTGTGTTAAG TTAACAGAGT GTTAACGTTC GGTTCCAAAT GCCAACGCCA TAGGAACAAA     720
ACAAACGTGT CCTCAAGTAA ACCCCTGCCG TTTACACCTC AATGGCTGCA TGGTGAAGCC     780
ATTAACACGT GGCGTAGGAT GCATGACGAC GCCATTGACA CCTGACTCTC TTCCCTTCTC     840
TTCATATATC TCTAATCAAT TCAACTACTC ATTGTCATAG CTATTCGGAA AATACATACA     900
CATCCTTTTC TCTTCGATCT CTCTCAATTC ACAAGAAGCA AAGTCGACGG ATCCCTGCAG     960
```

TAAATTACGC CATGACTATT TTCATAGTCC AATAAGGCTG ATGTCGGGAG TCCAGTTTAT 1020
GAGCAATAAG GTGTTTAGAA TTTGATCAAT GTTTATAATA AAAGGGGGAA GATGATATCA 1080
CAGTCTTTTG TTCTTTTGG CTTTGTAA ATTTGTGTGT TTCTATTTGT AAACCTCCTG 1140
TATATGTTGT ACTTCTTTCC CTTTTAAGT GGTATCGTCT ATATGGTAAA ACGTTATGTT 1200
TGGTCTTTCC TTTTCTCTGT TTAGGATAAA AAGACTGCAT GTTTTATCTT TAGTTATATT 1260
ATGTTGAGTA AATGAACTTT CATAGATCTG GTTCCGTAGA GTAGACTAGC AGCCGAGCTG 1320
AGCTGAACTG AACAGCTGGC AATGTGAACA CTGGATGCAA GATCAGATGT GAAGATCTCT 1380
AATATGGTGG TGGGATTGAA CATATCGTGT CTATATTTTT GTTGGCATTAGCTCTTAAC 1440
ATAGATATAA CTGATGCAGT CATTGGTTCA TACACATATA TAGTAAGGAA TTACAATGGC 1500
AACCCAACT TCAAAAACAG TAGGCCACCT GAATTGCCTT ATCGAATAAG AGTTTGTTTC 1560
CCCCCACTT ATGGGATGTA ATACATGGGA TTTGGGAGTT TGAATGAACG TTGAGACATG 1620
GCAGAACCTC TAGAGGTACC GGC GCGC 1647

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5 :

Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Lys
5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6 :

Val Pro Xaa Glu Pro Ser Ile Ala Ala Xaa
5 10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7 :

Glu Thr Tyr Val Pro Glu Glu Val Thr Lys
5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8 :

Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys
5 10

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9 :

Met Thr Asn Val Lys Pro Tyr Ile Pro Asp Phe
 5 10

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10 :

Phe Leu Pro Xaa Xaa Val Ala Ile Thr Gly Glu
 5 10

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11 :

Phe Gly Asn Thr Ser Ser Xaa Xaa Leu Tyr Xaa Glu Leu Ala Tyr Ala
 5 10 15
Lys

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12 :

Ala Glu Ala Glu Glu Val Met Tyr Gly Ala Ile Asp Glu Val Leu Glu
5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13 :

Xaa Asp Ile Ala Ile Ile Gly Ser Gly Ser Ala Gly Leu Ala Gln Ala
5 10 15

Xaa Ile Leu Lys Asp Ala Gly
20

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14 :

Gln Gln Phe Thr Val Trp Xaa Asn Ala Ser Glu Pro Ser
5 10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15 :

17

AAAYATHACNA CNYTNGG

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16 :

17

SWRTTRCAYT TRAANCC

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1810 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17 :

GAA ATG AGT AGG TCT AGC GAA CAA GAT CTA CTC TCT ACC GAG ATT GTT	48
Met Ser Arg Ser Ser Glu Gln Asp Leu Leu Ser Thr Glu Ile Val	
1 5 10 15	
AAC CGT GGG ATC GAA CCT TCC GGT CCA AAC GCC GGT TCA CCA ACG TTC	96
Asn Arg Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe	
20 25 30	
TCG GTC AGA GTC CGG AGA CGT TTA CCG GAT TTT CTT CAA TCC GTA AAC	144
Ser Val Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn	
35 40 45	
TTG AAG TAC GTG AAA CTT GGT TAT CAC TAC CTC ATA AAC CAT GCG GTT	192
Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val	
50 55 60	
TAC TTG GCG ACG ATA CCG GTT CTT GTG CTT GTG TTT AGT GCC GAA GTT	240
Tyr Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val	
65 70 75	
GGG AGT TTA AGC GGA GAA GAG ATT TGG AAG AAG CTT TGG GAC TAT GAT	288
Gly Ser Leu Ser Gly Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp	
80 85 90 95	
ATC GCA ACC GTC ATC GGA TTC TTC GGT GTC TTT GTC TTG ACC GTT TGC	336
Ile Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Val Cys	
100 105 110	

GTC	TAC	TTC	ATG	TCT	CGT	CCA	CGA	TCT	GTT	TAT	CTC	ATT	GAC	TTC	GCT	384
Val	Tyr	Phe	Met	Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Ile	Asp	Phe	Ala	
			115					120					125			
TGT	TTC	AAG	CCT	TCC	GAT	GAA	CTT	AAG	GTG	ACA	AGA	GAA	GAG	TTC	ATA	432
Cys	Phe	Lys	Pro	Ser	Asp	Glu	Leu	Lys	Val	Thr	Arg	Glu	Glu	Phe	Ile	
		130					135					140				
GAT	CTA	GCT	AGA	AAA	TCA	GGC	AAG	TTC	GAC	GAA	GAG	ATC	CTC	GGA	TTC	480
Asp	Leu	Ala	Arg	Lys	Ser	Gly	Lys	Phe	Asp	Glu	Glu	Ile	Leu	Gly	Phe	
	145					150						155				
AAG	AAG	AGG	ATC	CTT	CAA	GCC	TCA	GGA	ATA	GGC	GAT	GAA	ACG	TAC	GTC	528
Lys	Lys	Arg	Ile	Leu	Gln	Ala	Ser	Gly	Ile	Gly	Asp	Glu	Thr	Tyr	Val	
160					165					170					175	
CCA	AGA	TCA	ATC	TCT	TCG	TCG	GAA	AAC	ACA	ACA	ACG	ATG	AAA	GAA	GGT	576
Pro	Arg	Ser	Ile	Ser	Ser	Ser	Glu	Asn	Thr	Thr	Thr	Met	Lys	Glu	Gly	
				180					185					190		
CGT	GAA	GAA	GCC	TCG	ATG	ATG	ATA	TTC	GGC	GCA	CTC	GAC	GAA	CTC	TTC	624
Arg	Glu	Glu	Ala	Ser	Met	Met	Ile	Phe	Gly	Ala	Leu	Asp	Glu	Leu	Phe	
			195					200					205			
GAG	AAG	ACA	CGT	GTC	AAA	CCG	AAA	GAC	GTA	GGT	GTC	CTC	GTG	GTT	AAC	672
Glu	Lys	Thr	Arg	Val	Lys	Pro	Lys	Asp	Val	Gly	Val	Leu	Val	Val	Asn	
		210					215					220				
TGC	AGT	ATC	TTT	AAC	CCG	ACT	CCG	TCA	CTC	TCC	GCG	ATG	GTG	ATT	AAC	720
Cys	Ser	Ile	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Ile	Asn	
	225					230					235					
CAC	TAC	AAG	ATG	AGA	GGG	AAC	ATA	CTT	AGC	TAC	AAC	CTA	GGA	GGG	ATG	768
His	Tyr	Lys	Met	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Leu	Gly	Gly	Met	
240					245					250					255	
GGT	TGC	TCA	GCA	GGA	ATC	ATA	GCC	GTT	GAT	CTT	GCT	CGT	GAC	ATG	CTT	816
Gly	Cys	Ser	Ala	Gly	Ile	Ile	Ala	Val	Asp	Leu	Ala	Arg	Asp	Met	Leu	
				260					265					270		
CAG	TCT	AAC	CCG	AAT	AGT	TAC	GCG	GTG	GTT	GTG	AGT	ACC	GAG	ATG	GTT	864
Gln	Ser	Asn	Pro	Asn	Ser	Tyr	Ala	Val	Val	Val	Ser	Thr	Glu	Met	Val	
			275					280					285			

GGG Gly	TAT Tyr	AAT Asn 290	TGG Trp	TAC Tyr	GTG Val	GGA Gly	CGT Arg 295	GAC Asp	AAG Lys	TCA Ser	ATG Met 300	GTT Val	ATA Ile	CCT Pro	AAC Asn	912
TGC Cys 305	TTC Phe	TTT Phe	AGG Arg	ATG Met	GGT Gly	TGC Cys 310	TCC Ser	GCC Ala	GTT Val	ATG Met 315	CTG Leu	TCT Ser	AAC Asn	CGC Arg	CGC Arg	960
CGT Arg 320	GAC Asp	TTC Phe	CGC Arg	CAT His	GCT Ala 325	AAG Lys	TAC Tyr	CGC Arg	CTT Leu	GAG Glu 330	CAC His	ATT Ile	GTC Val	CGG Arg	ACT Thr 335	1008
CAC His	AAG Lys	GCT Ala	GCC Ala	GAC Asp 340	GAC Asp	CGT Arg	AGC Ser	TTC Phe	AGG Arg 345	AGT Ser	GTG Val	TAC Tyr	CAG Gln	GAA Glu 350	GAA Glu	1056
GAT Asp	GAA Glu	CAA Gln 355	GGA Gly	TTC Phe	AAG Lys	GGA Gly	TTA Leu	AAA Lys 360	ATA Ile	AGC Ser	AGA Arg	GAC Asp	CTA Leu 365	ATG Met	GAA Glu	1104
GTT Val	GGA Gly 370	GGT Gly	GAA Glu	GCT Ala	CTC Leu	AAG Lys	ACC Thr 375	AAC Asn	ATC Ile	ACC Thr	ACC Thr	TTA Leu 380	GGC Gly	CCT Pro	CTC Leu	1152
GTC Val 385	CTT Leu	CCT Pro	TTC Phe	TCC Ser	GAG Glu	CAG Gln 390	CTT Leu	CTC Leu	TTC Phe	TTT Phe 395	GCC Ala	GCT Ala	TTG Leu	ATC Ile	CGT Arg	1200
AGA Arg 400	ACT Thr	TTC Phe	TCA Ser	CCC Pro	GCC Ala 405	GCC Ala	AAA Lys	ACT Thr	ACC Thr	ACC Thr 410	ACC Thr	TCC Ser	TCC Ser	TCA Ser	GCC Ala 415	1248
ACT Thr	GCG Ala	AAA Lys	ATC Ile	AAC Asn 420	GGA Gly	GCC Ala	AAG Lys	TCG Ser	TCA Ser	TCC Ser 425	TCC Ser	TCT Ser	GAT Asp	CTA Leu 430	TCC Ser	1296
AAG Lys	CCG Pro	TAC Tyr 435	ATC Ile	CCG Pro	GAC Asp	TAC Tyr	AAG Lys	CTT Leu 440	GCC Ala	TTC Phe	GAG Glu	CAT His	TTC Phe 445	TGC Cys	TTC Phe	1344
CAC His	GCG Ala 450	GCA Ala	AGC Ser	AAA Lys	GCG Ala	GTG Val	CTT Leu 455	GAG Glu	GAG Glu	CTT Leu	CAG Gln	AAG Lys 460	AAT Asn	CTA Leu	GGC Gly	1392

TTG AGT GAT GAG AAC ATG GAG GCT TCT AAG ATG ACT TTA CAC AGG TTT	1440
Leu Ser Asp Glu Asn Met Glu Ala Ser Lys Met Thr Leu His Arg Phe	
465 470 475	
GGA AAC ACT TCC AGC AGT GGA ATC TGG TAC GAG CTT GCT TAC ATG GAG	1488
Gly Asn Thr Ser Ser Ser Gly Ile Trp Tyr Glu Leu Ala Tyr Met Glu	
480 485 490 495	
GCC AAG GAG AGT GTT CGT AGA GGC GAT AGG GTT TGG CAG ATT GCT TTT	1536
Ala Lys Glu Ser Val Arg Arg Gly Asp Arg Val Trp Gln Ile Ala Phe	
500 505 510	
GGG TCA GGT TTT AAG TGT AAC AGT GTG GTT TGG AAG GCA ATG AGG AAG	1584
Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys Ala Met Arg Lys	
515 520 525	
GTG AAG AAG CCG GCA AGG AAC AAT CCT TGG GTT GAT TGC ATT AAC CGT	1632
Val Lys Lys Pro Ala Arg Asn Asn Pro Trp Val Asp Cys Ile Asn Arg	
530 535 540	
TAC CCT GTC GCT CTC TGATCATTTA TTTTAAAT TATTATTTCT TCTTAATTAA	1687
Tyr Pro Val Ala Leu	
545	
ATCATCTATG ATCTCTCTTC CTGTGTTGTTG GATGATAGAC GTTTGTTTGC TGGTCATTCG	1747
TATCTTAAGA CTTCTATAAG AATGGATGGT TCAAGTCCAA AAAAAAAAAA AAAAAAAAAA	1807
AAA	1810

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18 :

GTCGACAAA	ATG	ACG	TCC	ATT	AAC	GTA	AAG	CTC	CTT	TAC	CAT	TAC	GTC	ATA	51	
	Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile		
	1				5					10						
ACC	AAC	CTT	TTC	AAC	CTT	TGT	TTC	TTT	CCA	TTA	ACG	GCG	ATC	GTC	GCC	99
Thr	Asn	Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	
15					20					25					30	
GGA	AAA	GCC	TAT	CGG	CTT	ACC	ATA	GAC	GAT	CTT	CAC	CAC	TTA	TAC	TAT	147
Gly	Lys	Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	
				35					40					45		
TCC	TAT	CTC	CAA	CAC	AAC	CTC	ATA	ACC	ATT	GCT	CCA	CTC	TTT	GCC	TTC	195
Ser	Tyr	Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	
			50					55					60			
ACC	GTT	TTC	GGT	TCG	GTT	CTC	TAC	ATC	GCA	ACC	CGG	CCC	AAA	CCG	GTT	243
Thr	Val	Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	
		65					70					75				
TAC	CTC	GTT	GAG	TAC	TCA	TGC	TAC	CTT	CCA	CCA	ACG	CAT	TGT	AGA	TCA	291
Tyr	Leu	Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	
	80					85					90					
AGT	ATC	TCC	AAG	GTC	ATG	GAT	ATC	TTT	TAC	CAA	GTA	AGA	AAA	GCT	GAT	339
Ser	Ile	Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	
95					100					105				110		
CCT	TCT	CGG	AAC	GGC	ACG	TGC	GAT	GAC	TCG	TCC	TGG	CTT	GAC	TTC	TTG	387
Pro	Ser	Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	
				115					120					125		
AGG	AAG	ATT	CAA	GAA	CGT	TCA	GGT	CTA	GGC	GAT	GAA	ACC	CAC	GGG	CCC	435
Arg	Lys	Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	
			130					135					140			
GAG	GGG	CTG	CTT	CAG	GTC	CCT	CCC	CGG	AAG	ACT	TTT	GCG	GCG	GCG	CGT	483
Glu	Gly	Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	
		145					150					155				

GAA Glu 160	GAG Glu	ACG Thr	GAG Glu	CAA Gln	GTT Val	ATC Ile 165	ATT Ile	GGT Gly	GCG Ala	CTA Leu 170	GAA Glu	AAT Asn	CTA Leu	TTC Phe	AAG Lys	531
AAC Asn 175	ACC Thr	AAT Asn	GTT Val	AAC Asn	CCT Pro 180	AAA Lys	GAT Asp	ATA Ile	GGT Gly	ATA Ile 185	CTT Leu	GTG Val	GTG Val	AAC Asn	TCA Ser 190	579
AGC Ser	ATG Met	TTT Phe	AAT Asn	CCA Pro 195	ACT Thr	CCT Pro	TCG Ser	CTC Leu	TCC Ser 200	GCG Ala	ATG Met	GTC Val	GTT Val	AAC Asn 205	ACT Thr	627
TTC Phe	AAG Lys	CTC Leu	CGA Arg 210	AGC Ser	AAC Asn	GTA Val	AGA Arg	AGC Ser 215	TTT Phe	AAC Asn	CTT Leu	GGT Gly	GGC Gly 220	ATG Met	GGT Gly	675
TGT Cys	AGT Ser	GCC Ala 225	GGC Gly	GTT Val	ATA Ile	GCC Ala 230	ATT Ile	GAT Asp	CTA Leu	GCA Ala	AAG Lys	GAC Asp 235	TTG Leu	TTG Leu	CAT His	723
GTC Val 240	CAT His	AAA Lys	AAT Asn	ACG Thr	TAT Tyr	GCT Ala 245	CTT Leu	GTG Val	GTG Val	AGC Ser	ACA Thr 250	GAG Glu	AAC Asn	ATC Ile	ACT Thr	771
TAT Tyr 255	AAC Asn	ATT Ile	TAC Tyr	GCT Ala	GGT Gly 260	GAT Asp	AAT Asn	AGG Arg	TCC Ser	ATG Met 265	ATG Met	GTT Val	TCA Ser	AAT Asn	TGC Cys 270	819
TTG Leu	TTC Phe	CGT Arg	GTT Val	GGT Gly 275	GGG Gly	GCC Ala	GCT Ala	ATT Ile	TTG Leu 280	CTC Leu	TCC Ser	AAC Asn	AAG Lys	CCT Pro 285	AGA Arg	867
GAT Asp	CGT Arg	AGA Arg	CGG Arg	TCC Ser	AAG Lys	TAC Tyr	GAG Glu	CTA Leu 295	GTT Val	CAC His	ACG Thr	GTT Val	CGA Arg 300	ACG Thr	CAT His	915
ACC Thr	GGA Gly 305	GCT Ala	GAC Asp	GAC Asp	AAG Lys	TCT Ser	TTT Phe 310	CGT Arg	TGC Cys	GTG Val	CAA Gln 315	CAA Gln	GGA Gly	GAC Asp	GTT Val	963
GAG Glu 320	AAC Asn	GGC Gly	AAA Lys	ACC Thr	GGA Gly	GTG Val 325	AGT Ser	TTG Leu	TCC Ser	AAG Lys	GAC Asp 330	ATA Ile	ACC Thr	GAT Asp	GTT Val	1011

GCT	GGT	CGA	ACG	GTT	AAG	AAA	AAC	ATA	GCA	ACG	CTG	GGT	CCG	TTG	ATT	1059
Ala	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	
335					340					345					350	
CTT	CCG	TTA	AGC	GAG	AAA	CTT	CTT	TTT	TTC	GTT	ACC	TTC	ATG	GGC	AAG	1107
Leu	Pro	Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	
				355					360					365		
AAA	CTT	TTC	AAA	GAC	AAA	ATC	AAA	CAT	TAT	TAC	GTC	CCG	GAC	TTC	AAG	1155
Lys	Leu	Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	
			370					375					380			
CTT	GCT	ATC	GAC	CAT	TTT	TGT	ATA	CAT	GCC	GGA	GGC	AAA	GCC	GTG	ATT	1203
Leu	Ala	Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Lys	Ala	Val	Ile	
		385					390					395				
GAT	GTG	CTA	GAG	AAG	AAC	CTA	GGC	CTA	GCA	CCG	ATC	GAT	GTA	GAG	GCA	1251
Asp	Val	Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	
	400					405					410					
TCA	AGA	TCA	ACG	TTA	CAT	AGA	TTT	GGA	AAC	ACT	TCA	TCT	AGC	TCA	ATA	1299
Ser	Arg	Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	
415					420					425					430	
TGG	TAT	GAG	TTG	GCA	TAC	ATA	GAA	GCA	AAA	GGA	AGG	ATG	AAG	AAA	GGT	1347
Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	
			435					440						445		
AAT	AAA	GTT	TGG	CAG	ATT	GCT	TTA	GGG	TCA	GGC	TTT	AAG	TGT	AAC	AGT	1395
Asn	Lys	Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	
			450					455					460			
GCA	GTT	TGG	GTG	GCT	CTA	AAC	AAT	GTC	AAA	GCT	TCC	AAA	TAGGATCC			1442
Ala	Val	Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Lys				
		465				470						475				

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19 :

GTCGACAAA	ATG	ACG	TCC	ATT	AAC	GTA	AAG	CTC	CTT	TAC	CAT	TAC	GTC	ATA	51	
	Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile		
	1				5					10						
ACC	AAC	CTT	TTC	AAC	CTT	TGC	TTC	TTT	CCG	TTA	ACG	GCG	ATC	GTC	GCC	99
Thr	Asn	Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	
15					20					25					30	
GGA	AAA	GCC	TAT	CGG	CTT	ACC	ATA	GAC	GAT	CTT	CAC	CAC	TTA	TAC	TAT	147
Gly	Lys	Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	
				35					40					45		
TCC	TAT	CTC	CAA	CAC	AAC	CTC	ATA	ACC	ATC	GCT	CCA	CTC	TTT	GCC	TTC	195
Ser	Tyr	Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	
			50					55					60			
ACC	GTT	TTC	GGT	TCG	GTT	CTC	TAC	ATC	GCA	ACC	CGG	CCC	AAA	CCG	GTT	243
Thr	Val	Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	
		65					70					75				
TAC	CTC	GTT	GAG	TAC	TCA	TGC	TAC	CTT	CCA	CCA	ACG	CAT	TGT	AGA	TCA	291
Tyr	Leu	Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	
	80					85					90					
AGT	ATC	TCC	AAG	GTC	ATG	GAT	ATC	TTT	TAT	CAA	GTA	AGA	AAA	GCT	GAT	339
Ser	Ile	Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	
95					100					105					110	
CCT	TCT	CGG	AAC	GGC	ACG	TGC	GAT	GAC	TCG	TCG	TGG	CTT	GAC	TTC	TTG	387
Pro	Ser	Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	
				115					120					125		

AGG	AAG	ATT	CAA	GAA	CGT	TCA	GGT	CTA	GGC	GAT	GAA	ACT	CAC	GGG	CCC	435
Arg	Lys	Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	
			130					135					140			
GAG	GGG	CTG	CTT	CAG	GTC	CCT	CCC	CGG	AAG	ACT	TTT	GCG	GCG	GCG	CGT	483
Glu	Gly	Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	
		145					150					155				
GAA	GAG	ACG	GAG	CAA	GTT	ATC	ATT	GGT	GCG	CTA	GAA	AAT	CTA	TTC	AAG	531
Glu	Glu	Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	
	160					165					170					
AAC	ACC	AAC	GTT	AAC	CCT	AAA	GAT	ATA	GGT	ATA	CTT	GTG	GTG	AAC	TCA	579
Asn	Thr	Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	
175					180					185					190	
AGC	ATG	TTT	AAT	CCA	ACT	CCA	TCG	CTC	TCC	GCG	ATG	GTC	GTT	AAC	ACT	627
Ser	Met	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	
				195					200					205		
TTC	AAG	CTC	CGA	AGC	AAC	GTA	AGA	AGC	TTT	AAC	CTT	GGT	GGC	ATG	GGT	675
Phe	Lys	Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	
			210					215					220			
TGT	AGT	GCC	GGC	GTT	ATA	GCC	ATT	GAT	CTA	GCA	AAG	GAC	TTG	TTG	CAT	723
Cys	Ser	Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	
		225					230					235				
GTC	CAT	AAA	AAT	ACG	TAT	GCT	CTT	GTG	GTG	AGC	ACA	GAG	AAC	ATC	ACT	771
Val	His	Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	
	240					245					250					
TAT	AAC	ATT	TAC	GCT	GGT	GAT	AAT	AGG	TCC	ATG	ATG	GTT	TCA	AAT	TGC	819
Tyr	Asn	Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	
255					260					265					270	
TTG	TTC	CGT	GTT	GGT	GGG	GCC	GCT	ATT	TTG	CTC	TCC	AAC	AAG	CCT	GGA	867
Leu	Phe	Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	
				275					280					285		
GAT	CGT	AGA	CGG	TCC	AAG	TAC	GAG	CTA	GTT	CAC	ACG	GTT	CGA	ACG	CAT	915
Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	
			290					295					300			

ACC	GGA	GCT	GAC	GAC	AAG	TCT	TTT	CGT	TGC	GTG	CAA	CAA	GGA	GAC	GAT	963
Thr	Gly	Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	
		305					310					315				
GAG	AAC	GGC	AAA	ATC	GGA	GTG	AGT	TTG	TCC	AAG	GAC	ATA	ACC	GAT	GTT	1011
Glu	Asn	Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	
	320					325					330					
GCT	GGT	CGA	ACG	GTT	AAG	AAA	AAC	ATA	GCA	ACG	TTG	GGT	CCG	TTG	ATT	1059
Ala	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	
335					340					345					350	
CTT	CCG	TTA	AGC	GAG	AAA	CTT	CTT	TTT	TTC	GTT	ACC	TTC	ATG	GGC	AAG	1107
Leu	Pro	Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	
				355					360					365		
AAA	CTT	TTC	AAA	GAT	AAA	ATC	AAA	CAT	TAC	TAC	GTC	CCG	GAT	TTC	AAA	1155
Lys	Leu	Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	
			370					375					380			
CTT	GCT	ATT	GAC	CAT	TTT	TGT	ATA	CAT	GCC	GGA	GGC	AGA	GCC	GTG	ATT	1203
Leu	Ala	Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	
		385					390					395				
GAT	GTG	CTA	GAG	AAG	AAC	CTA	GCC	CTA	GCA	CCG	ATC	GAT	GTA	GAG	GCA	1251
Asp	Val	Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	
	400					405					410					
TCA	AGA	TCA	ACG	TTA	CAT	AGA	TTT	GGA	AAC	ACT	TCA	TCT	AGC	TCA	ATA	1299
Ser	Arg	Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	
415					420					425					430	
TGG	TAT	GAG	TTG	GCA	TAC	ATA	GAA	GCA	AAA	GGA	AGG	ATG	AAG	AAA	GGT	1347
Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	
				435					440					445		
AAT	AAA	GTT	TGG	CAG	ATT	GCT	TTA	GGG	TCA	GGC	TTT	AAG	TGT	AAC	AGT	1395
Asn	Lys	Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	
			450					455					460			

GCA	GTT	TGG	GTG	GCT	CTA	AAC	AAT	GTC	AAA	GCT	TCC	AAA	TAGGATCC	1442
Ala	Val	Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Lys		
		465					470					475		

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20 :

AAG	CTT	AAA	CTA	GTG	TAT	CAT	TAC	CTA	ATC	TCC	AAC	GCT	CTC	TAC	ATC	48
Lys	Leu	Lys	Leu	Val	Tyr	His	Tyr	Leu	Ile	Ser	Asn	Ala	Leu	Tyr	Ile	
1				5					10					15		

CTC	CTC	CTT	CCT	CTC	CTC	GCC	GCA	ACA	ATC	GCT	AAC	CTC	TCT	TCT	TTC	96
Leu	Leu	Leu	Pro	Leu	Leu	Ala	Ala	Thr	Ile	Ala	Asn	Leu	Ser	Ser	Phe	
			20					25					30			

ACC	ATC	AAC	GAC	CTC	TCT	CTC	CTC	TAC	AAC	ACA	CTC	CGT	TTC	CAT	TTC	144
Thr	Ile	Asn	Asp	Leu	Ser	Leu	Leu	Tyr	Asn	Thr	Leu	Arg	Phe	His	Phe	
		35					40					45				

CTC	TCC	GCC	ACA	CTC	GCC	ACC	GCA	CTC	TTG	ATC	TCT	CTC	TCC	ACC	GCT	192
Leu	Ser	Ala	Thr	Leu	Ala	Thr	Ala	Leu	Leu	Ile	Ser	Leu	Ser	Thr	Ala	
	50					55					60					

TAC	TTC	ACC	ACC	CGT	CCT	CGC	CGT	GTC	TTC	CTC	CTC	GAC	TTC	TCG	TGT	240
Tyr	Phe	Thr	Thr	Arg	Pro	Arg	Arg	Val	Phe	Leu	Leu	Asp	Phe	Ser	Cys	
65					70				75						80	

TAC	AAA	CCA	GAC	CCT	TCA	CTG	ATC	TGC	ACT	CGT	GAA	ACA	TTC	ATG	GAC	288
Tyr	Lys	Pro	Asp	Pro	Ser	Leu	Ile	Cys	Thr	Arg	Glu	Thr	Phe	Met	Asp	
				85				90						95		

AGA	TCT	CAA	CGT	GTA	GGC	ATC	TTC	ACA	GAA	GAC	AAC	TTA	GCT	TTC	CAA	336
Arg	Ser	Gln	Arg	Val	Gly	Ile	Phe	Thr	Glu	Asp	Asn	Leu	Ala	Phe	Gln	
			100					105					110			
CAA	AAG	ATC	CTC	GAA	AGA	TCC	GGT	CTA	GGT	CAG	AAA	ACT	TAC	TTC	CCT	384
Gln	Lys	Ile	Leu	Glu	Arg	Ser	Gly	Leu	Gly	Gln	Lys	Thr	Tyr	Phe	Pro	
		115					120					125				
GAA	GCT	CTT	CTT	CGT	GTT	CCT	CCT	AAT	CCT	TGT	ATG	GAA	GAA	GCG	AGA	432
Glu	Ala	Leu	Leu	Arg	Val	Pro	Pro	Asn	Pro	Cys	Met	Glu	Glu	Ala	Arg	
	130					135					140					
AAA	GAG	GCA	GAA	ACA	GTT	ATG	TTC	GGA	GCT	ATT	GAC	GCG	GTT	CTT	GAG	480
Lys	Glu	Ala	Glu	Thr	Val	Met	Phe	Gly	Ala	Ile	Asp	Ala	Val	Leu	Glu	
145					150					155					160	
AAG	ACC	GGT	GTG	AAA	CCT	AAA	GAT	ATT	GGA	ATC	CTT	GTG	GTG	AAT	TGT	528
Lys	Thr	Gly	Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	
				165					170					175		
AGC	TTG	TTT	AAT	CCA	ACA	CCG	TCA	CTT	TCT	GCT	ATG	ATT	GTG	AAT	AAG	576
Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	
			180					185					190			
TAT	AAG	CTT	AGA	GGC	AAC	ATT	TTG	AGC	TAT	AAT	TTC	GGC	GGG	ATG	GG	623
Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Phe	Gly	Gly	Met	Gly	
		195					200					205				

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21 :

AAG	CTT	AAG	TTA	GGC	TAC	CAC	TAT	CTG	ATC	ACT	CAC	TTT	TTT	AAA	CTC	48
Lys	Leu	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	Thr	His	Phe	Phe	Lys	Leu	
1				5				10						15		
ATG	TTC	CTC	CCT	CTA	ATG	GCT	GTT	TTG	TTC	ATG	AAT	GTC	TCA	TTG	TTA	96
Met	Phe	Leu	Pro	Leu	Met	Ala	Val	Leu	Phe	Met	Asn	Val	Ser	Leu	Leu	
			20					25					30			
AGC	CTA	AAC	CAT	CTT	CAG	CTC	TAT	TAC	AAT	TCC	ACC	GGA	TTC	ATC	TTC	144
Ser	Leu	Asn	His	Leu	Gln	Leu	Tyr	Tyr	Asn	Ser	Thr	Gly	Phe	Ile	Phe	
		35					40					45				
GTC	ATC	ACT	CTC	GCC	ATT	GTC	GGA	TCC	ATT	GTC	TTC	TTC	ATG	TCT	CGA	192
Val	Ile	Thr	Leu	Ala	Ile	Val	Gly	Ser	Ile	Val	Phe	Phe	Met	Ser	Arg	
	50					55					60					
CCT	AGA	TCC	ATC	TAC	CTT	CTA	GAT	TAC	TCT	TGC	TAC	CTC	CCG	CCT	TCG	240
Pro	Arg	Ser	Ile	Tyr	Leu	Leu	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Ser	
65					70					75					80	
AGT	CAA	AAA	GTT	AGC	TAC	CAG	AAA	TTC	ATG	AAC	AAC	TCT	AGT	TTG	ATT	288
Ser	Gln	Lys	Val	Ser	Tyr	Gln	Lys	Phe	Met	Asn	Asn	Ser	Ser	Leu	Ile	
				85				90						95		
CAA	GAT	TTC	AGC	GAA	ACT	TCT	CTT	GAG	TTC	CAG	AGG	AAG	ATC	TTG	ATT	336
Gln	Asp	Phe	Ser	Glu	Thr	Ser	Leu	Glu	Phe	Gln	Arg	Lys	Ile	Leu	Ile	
			100					105					110			
CGC	TCT	GGT	CTC	GGT	GAA	GAG	ACT	TAT	TTA	CCG	GAT	TCT	ATT	CAC	TCT	384
Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	Pro	Asp	Ser	Ile	His	Ser	
		115					120					125				
ATC	CCT	CCG	CGT	CCT	ACT	ATG	GCT	GCA	GCG	CGT	GAA	GAA	GCG	GAG	CAG	432
Ile	Pro	Pro	Arg	Pro	Thr	Met	Ala	Ala	Ala	Arg	Glu	Glu	Ala	Glu	Gln	
	130					135					140					
GTA	ATC	TTC	GGT	GCA	CTC	GAC	AAT	CTT	TTC	GAG	AAT	ACA	AAA	ATC	AAT	480
Val	Ile	Phe	Gly	Ala	Leu	Asp	Asn	Leu	Phe	Glu	Asn	Thr	Lys	Ile	Asn	
145					150					155					160	

CCT	AGG	GAG	ATT	GGT	GTT	CTT	GTT	GTG	AAT	TGT	AGT	TTG	TTT	AAC	CCC	528
Pro	Arg	Glu	Ile	Gly	Val	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	Asn	Pro	
				165					170					175		

ACG	CCT	TCT	TTA	TCC	GCC	ATG	ATT	GTT	AAC	AAG	TAT	AAG	CTT	AGA	GGA	576
Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	Arg	Gly	
			180					185					190			

AAC	ATT	AAG	AGC	TTT	AAT	CTC	GGC	GGC	ATG	G						607
Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met							
		195					200									

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 622 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAG	CTT	AAA	CTG	GGG	TAC	CAC	TAC	CTC	ATT	ACT	CAT	CTC	TTC	AAG	CTC	48
Lys	Leu	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	Thr	His	Leu	Phe	Lys	Leu	
1				5				10						15		
TGT	TTG	GTT	CCA	TTA	ATG	GCG	GTT	TTA	GTC	ACA	GAG	ATC	TCC	CGA	TTA	96
Cys	Leu	Val	Pro	Leu	Met	Ala	Val	Leu	Val	Thr	Glu	Ile	Ser	Arg	Leu	
			20					25					30			
ACA	ACA	GAC	GAT	CTT	TAC	CAG	ATT	TGC	CTT	CAT	CTC	CAA	TAC	AAT	CTC	144
Thr	Thr	Asp	Asp	Leu	Tyr	Gln	Ile	Cys	Leu	His	Leu	Gln	Tyr	Asn	Leu	
		35					40					45				
GTT	GCT	TTC	ATC	TTT	CTC	TCT	GCT	TTA	GCT	ATC	TTT	GGC	TCC	ACC	GTT	192
Val	Ala	Phe	Ile	Phe	Leu	Ser	Ala	Leu	Ala	Ile	Phe	Gly	Ser	Thr	Val	
	50					55					60					
TAC	ATC	ATG	AGT	CGT	CCC	AGA	TCT	GTT	TAT	CTC	GTT	GAT	TAC	TCT	TGT	240
Tyr	Ile	Met	Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Val	Asp	Tyr	Ser	Cys	
65					70					75					80	
TAT	CTT	CCT	CCG	GAG	AGT	CTT	CAG	GTT	AAG	TAT	CAG	AAG	TTT	ATG	GAT	288
Tyr	Leu	Pro	Pro	Glu	Ser	Leu	Gln	Val	Lys	Tyr	Gln	Lys	Phe	Met	Asp	
				85				90						95		
CAT	TCT	AAG	TTG	ATT	GAA	GAT	TTC	AAT	GAG	TCA	TCT	TTA	GAG	TTT	CAG	336
His	Ser	Lys	Leu	Ile	Glu	Asp	Phe	Asn	Glu	Ser	Ser	Leu	Glu	Phe	Gln	
			100					105					110			
AGG	AAG	ATT	CTT	GAA	CGT	TCT	GGT	TTA	GGA	GAA	GAG	ACT	TAT	CTC	CCT	384
Arg	Lys	Ile	Leu	Glu	Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	Pro	
		115					120					125				
GAA	GCT	TTA	CAT	TGT	ATC	CCT	CCG	AGG	CCT	ACG	ATG	ATG	GCG	GCT	CGT	432
Glu	Ala	Leu	His	Cys	Ile	Pro	Pro	Arg	Pro	Thr	Met	Met	Ala	Ala	Arg	
	130					135					140					
GAG	GAA	GCT	GAG	CAG	GTA	ATG	TTT	GGT	GCT	CTT	GAT	AAG	CTT	TTC	GAG	480
Glu	Glu	Ala	Glu	Gln	Val	Met	Phe	Gly	Ala	Leu	Asp	Lys	Leu	Phe	Glu	
145				150						155					160	

AAT	ACC	AAG	ATT	AAC	CCT	AGG	GAT	ATT	GGT	GTG	TTG	GTT	GTG	AAT	TGT	528
Asn	Thr	Lys	Ile	Asn	Pro	Arg	Asp	Ile	Gly	Val	Leu	Val	Val	Asn	Cys	
				165					170					175		

AGC	TTG	TTT	AAT	CCT	ACA	CCT	TCG	TTG	TCA	GCT	ATG	ATT	GTT	AAC	AAG	576
Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	
			180					185					190			

TAT	AAG	CTT	AGA	GGG	AAT	GTT	AAG	AGT	TTT	AAC	CTG	GGG	GGC	ATT	G	622
Tyr	Lys	Leu	Arg	Gly	Asn	Val	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Ile		
		195					200					205				

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23 :

AAG	CTT	AAG	TTA	TGG	TAT	CAC	TAC	CTG	ATT	TCT	CAC	CTT	TTT	AAG	CTC	48
Lys	Leu	Lys	Leu	Trp	Tyr	His	Tyr	Leu	Ile	Ser	His	Leu	Phe	Lys	Leu	
1				5					10					15		

TTG	TTG	GTT	CCT	TTA	ATG	GCG	GTT	CTG	TTC	ACG	AAT	GTC	TCC	CGG	TTA	96
Leu	Leu	Val	Pro	Leu	Met	Ala	Val	Leu	Phe	Thr	Asn	Val	Ser	Arg	Leu	
			20					25					30			

AGC	CTA	AAC	CAG	CTC	TGT	CTC	GAT	CTC	TCT	CTC	CAG	CTC	CAG	TTC	AAT	144
Ser	Leu	Asn	Gln	Leu	Cys	Leu	Asp	Leu	Ser	Leu	Gln	Leu	Gln	Phe	Asn	
		35					40					45				

CTC	GTC	GGA	TTC	ATC	TTC	TTC	ATT	ACC	GTC	TCC	ATT	TTC	GGA	TTC	ACA	192
Leu	Val	Gly	Phe	Ile	Phe	Phe	Ile	Thr	Val	Ser	Ile	Phe	Gly	Phe	Thr	
	50					55				60						

GTT	ATC	TTC	ATG	TCC	CGA	CCT	AGA	TCC	GTT	TAC	CTC	CTC	GAC	TAC	TCA	240
Val	Ile	Phe	Met	Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Leu	Asp	Tyr	Ser	
65					70					75					80	

TGT	TAC	CTC	CCG	CCG	TCG	AAT	CTC	AAA	GTT	AGC	TAC	CAG	ACA	TTC	ATG	288
Cys	Tyr	Leu	Pro	Pro	Ser	Asn	Leu	Lys	Val	Ser	Tyr	Gln	Thr	Phe	Met	
			85						90					95		
AAT	CAT	TCT	AAA	CTG	ATT	GAA	GAT	TTC	GAC	GAG	TCG	TCG	CTT	GAG	TTC	336
Asn	His	Ser	Lys	Leu	Ile	Glu	Asp	Phe	Asp	Glu	Ser	Ser	Leu	Glu	Phe	
			100					105					110			
CAG	CGG	AAG	ATC	CTG	AAG	CGA	TCC	GGT	CTC	GGC	GAA	GAG	ACT	TAC	CTC	384
Gln	Arg	Lys	Ile	Leu	Lys	Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	
		115					120						125			
CCG	GAA	TCT	ATC	CAC	TGC	ATC	CCG	CCG	CGT	CCG	ACT	ATG	GCG	GCG	GCG	432
Pro	Glu	Ser	Ile	His	Cys	Ile	Pro	Pro	Arg	Pro	Thr	Met	Ala	Ala	Ala	
	130					135					140					
CGT	GAG	GAA	TCG	GAG	CAG	GTA	ATC	TTC	GGT	GCA	CTC	GAC	AAT	CTC	TTC	480
Arg	Glu	Glu	Ser	Glu	Gln	Val	Ile	Phe	Gly	Ala	Leu	Asp	Asn	Leu	Phe	
145					150					155					160	
GAG	AAT	ACC	AAA	ATC	GAC	CCT	AGG	GAG	ATT	GGT	GTT	GTG	GTG	GTG	AAC	528
Glu	Asn	Thr	Lys	Ile	Asp	Pro	Arg	Glu	Ile	Gly	Val	Val	Val	Val	Asn	
				165					170					175		
TGC	AGC	TTG	TTT	AAC	CCG	ACG	CCT	TCT	TTA	TCC	GCC	ATG	ATT	GTG	AAC	576
Cys	Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	
			180					185					190			
AAG	TAT	AAG	CTT	AGA	GGA	AAC	GTG	AAG	AGC	TTT	AAT	CTC	GGT	GGC	ATG	G 625
Lys	Tyr	Lys	Leu	Arg	Gly	Asn	Val	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	
		195					200					205				

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

CTG AAG CGA TCC GGT CTC GGC GAA GAG ACT TAC CTC CCG GAA TCT ATC	488
Leu Lys Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro Glu Ser Ile	
135 140 145	
CAC TGC ATC CCG CCG CGT CCG ACT ATG GCG GCG GCG CGT GAG GAA TCG	536
His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Arg Glu Glu Ser	
150 155 160 165	
GAG CAG GTA ATC TTC GGT GCA CTC GAC AAT CTC TTC GAG AAT ACC AAA	584
Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Glu Asn Thr Lys	
170 175 180	
ATC GAC CCT AGG GAG ATT GGT GTT GTG GTG GTG AAC TGC AGC TTG TTT	632
Ile Asp Pro Arg Glu Ile Gly Val Val Val Val Asn Cys Ser Leu Phe	
185 190 195	
AAC CCG ACG CCT TCT TTA TCC GCC ATG ATT GTG AAC AAG TAT AAG CTT	680
Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu	
200 205 210	
AGA GGA AAC GTG AAG AGC TTT AAC CTC GGA GGA ATG GGA TGT AGG GCT	728
Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Arg Ala	
215 220 225	
GGT GTC ATC GCC GTT GAT CTC GCT AAT GAC ATT TTA CAG CTC CAT AGA	776
Gly Val Ile Ala Val Asp Leu Ala Asn Asp Ile Leu Gln Leu His Arg	
230 235 240 245	
AAC ACA TTA GCT CTT GTG GTT AGC ACA GAG AAC ATC ACT CAG AAT TGG	824
Asn Thr Leu Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn Trp	
250 255 260	
TAC TTT GGT AAC AAC AAA GCA ATG TTG ATT CCT AAT TGC TTG TTT AGG	872
Tyr Phe Gly Asn Asn Lys Ala Met Leu Ile Pro Asn Cys Leu Phe Arg	
265 270 275	
GTT GGT GGA TCC GCG GTT CTG CTT TCG AAC AAG CCT CGT GAT CGA AAA	920
Val Gly Gly Ser Ala Val Leu Leu Ser Asn Lys Pro Arg Asp Arg Lys	
280 285 290	
CGA TCC AAG TAT AAA CTT GTT CAC ACG GTA CGG ACT CAT AAA GGA TCT	968
Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Lys Gly Ser	
295 300 305	

GAT	GAG	AAA	GCA	TTC	AAC	TGT	GTG	TAC	CAA	GAA	CAA	GAC	GAG	GAC	TTG	1016
Asp	Glu	Lys	Ala	Phe	Asn	Cys	Val	Tyr	Gln	Glu	Gln	Asp	Glu	Asp	Leu	
310					315					320					325	
AAA	ACC	GGA	GTT	TCT	TTG	TCT	AAA	GAC	CTA	ATG	TCT	ATA	GCT	GGA	GAA	1064
Lys	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	Leu	Met	Ser	Ile	Ala	Gly	Glu	
				330					335					340		
GCT	CTA	AAG	ACA	AAT	ATC	ACC	ACT	TTG	GGT	CCT	CTG	GTT	CTT	CCA	ATA	1112
Ala	Leu	Lys	Thr	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	Ile	
			345					350					355			
AGC	GAG	CAG	ATT	CTG	TTC	ATT	GCG	ACT	TTT	GTT	GCA	AAG	AGA	TTG	TTC	1160
Ser	Glu	Gln	Ile	Leu	Phe	Ile	Ala	Thr	Phe	Val	Ala	Lys	Arg	Leu	Phe	
		360					365					370				
AGT	GCC	AAG	AAG	AAG	AAG	AAG	AAG	CCT	TAC	ATA	CCG	GAT	TTC	AAG	CTT	1208
Ser	Ala	Lys	Lys	Lys	Lys	Lys	Lys	Pro	Tyr	Ile	Pro	Asp	Phe	Lys	Leu	
	375						380				385					
GCC	TTT	GAT	CAT	TTC	TGT	ATT	CAC	GCA	GGA	GGT	AGA	GCC	GTG	ATC	GAT	1256
Ala	Phe	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	
390					395					400					405	
GAA	CTA	GAG	AAG	AGT	TTA	AAG	CTA	TTG	CCA	AAA	CAT	GTG	GAG	GCT	TCT	1304
Glu	Leu	Glu	Lys	Ser	Leu	Lys	Leu	Leu	Pro	Lys	His	Val	Glu	Ala	Ser	
				410					415					420		
AGA	ATG	ACA	TTG	CAT	AGA	TTT	GGA	AAC	ACT	TCA	TCG	AGC	TCT	ATT	TGG	1352
Arg	Met	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	
			425					430					435			
TAT	GAA	TTA	GCT	TAC	ACA	GAA	GCT	AAA	GGA	AGA	ATG	AGA	AAA	GGG	AAT	1400
Tyr	Glu	Leu	Ala	Tyr	Thr	Glu	Ala	Lys	Gly	Arg	Met	Arg	Lys	Gly	Asn	
		440					445					450				
CGA	GTT	TGG	CAG	ATT	GCT	TTT	GGA	AGC	GGC	TTT	AAG	TGT	AAC	AGC	GCG	1448
Arg	Val	Trp	Gln	Ile	Ala	Phe	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	
	455					460					465					

GTT TGG GTG GCT CTT CGT GAT GTC GAG CCC TCG GTT AAC AAT CCT TGG 1496
 Val Trp Val Ala Leu Arg Asp Val Glu Pro Ser Val Asn Asn Pro Trp
 470 475 480 485

GAA CAT TGC ATC CAT AGA TAT CCG GTT AAG ATC GAT CTC TGATTTCAGC 1545
 Glu His Cys Ile His Arg Tyr Pro Val Lys Ile Asp Leu
 490 495

TTAACCGGTA AAATTGGTCT GTACATATAT TTACCACTGA GTAAAGACAT CAGTTAATGA 1605

TTTGTGTGTTA CTCAATTGGG CTAAGTGTAT TATTATATGT GTTGTATATA ATAAAGGTAG 1665

AACGTAAATT TACTAAGAAA AAAAAAAAAA AAAAAAAAAA 1704

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1664 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CA ATG ACG TCT GTG AAC GTA AAA CTC CTT TAC CAT TAC GTC ATA ACC 47
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr
 1 5 10 15

AAC TTT TTC AAC CTC TGT TTC TTC CCA CTG ACG GGG ATC CTC GCC GGA 95
 Asn Phe Phe Asn Leu Cys Phe Phe Pro Leu Thr Gly Ile Leu Ala Gly
 20 25 30

AAA GGC TCT CGT CTT ACC ACA AAC GAT CTC CAC CAC TTC TAT TCA TAT 143
 Lys Gly Ser Arg Leu Thr Thr Asn Asp Leu His His Phe Tyr Ser Tyr
 35 40 45

CTC CAA CAC AAN CTT ATA ACC TTA ACC CTA CTC TTT GGC TTC ACC GTT	191
Leu Gln His Xxx Leu Ile Thr Leu Thr Leu Leu Phe Gly Phe Thr Val	
50 55 60	
TTT GGT TCG GTT CTC TAC TTC GTA ANC CGA CCC AAA CCG GTT TAC CTC	239
Phe Gly Ser Val Leu Tyr Phe Val Xxx Arg Pro Lys Pro Val Tyr Leu	
65 70 75	
GTT GAC TAC TCC TGC TAC CTT CCA CCA CAA CAT CTT AGC GCT GGT ATC	287
Val Asp Tyr Ser Cys Tyr Leu Pro Pro Gln His Leu Ser Ala Gly Ile	
80 85 90 95	
TCT AAG ACC ATG GAA ATC TTT TAT CAA ATA AGA AAA TCT GAT CCT TTA	335
Ser Lys Thr Met Glu Ile Phe Tyr Gln Ile Arg Lys Ser Asp Pro Leu	
100 105 110	
CGA AAC GTG GCA TTA GAT GAT TCG TCT TCT CTT GAT TTC TTG AGA AAG	383
Arg Asn Val Ala Leu Asp Asp Ser Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
ATT CAA GAG CGT TCA GGT CTA GGC GAT GAA ACC TAC GGC CCC GAG GGA	431
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Gly Pro Glu Gly	
130 135 140	
CTG TTT GAG ATT CCT CCG AGG AAG AAT TTA GCG TCG GCG CGT GAA GAG	479
Leu Phe Glu Ile Pro Pro Arg Lys Asn Leu Ala Ser Ala Arg Glu Glu	
145 150 155	
ACG GAG CAA GTA ATC AAC GGT GCG CTA AAA AAT CTA TTC GAG AAC AAC	527
Thr Glu Gln Val Ile Asn Gly Ala Leu Lys Asn Leu Phe Glu Asn Asn	
160 165 170 175	
AAA GTT AAC CCT AAA GAG ATT GGT ATA CTT GTG GTG AAC TCA AGC ATG	575
Lys Val Asn Pro Lys Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
TTT AAT CCG ACT CCT TCG TTA TCC GCG ATG GTA GTT AAT ACT TCC AAG	623
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Ser Lys	
195 200 205	

CTC	CGA	AGC	AAC	ATC	AAA	AGC	TTT	AAT	CTT	GGA	GGA	ATG	GGT	TGC	AGT	671
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
		210					215					220				
GCT	GGT	GTT	ATC	GCC	ATT	GAT	CTA	GCT	AAA	GAC	TTG	TTG	CAT	GTT	CAT	719
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
	225					230					235					
AAA	AAC	ACA	TAT	GCT	CTT	GTG	GTG	AGC	ACA	GAG	AAC	ATC	ACT	CAA	AAC	767
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Asn	
240					245					250					255	
ATT	TAT	ACC	GGT	GAT	AAC	AGA	TCC	ATG	ATG	GTT	TCG	AAT	TGC	TTG	TTC	815
Ile	Tyr	Thr	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	
				260					265					270		
CGT	GTC	GGT	GGG	GCA	GCG	ATT	CTG	CTC	TCC	AAC	AAG	CCG	GGG	GAT	CGA	863
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
			275				280						285			
AGA	CGG	TCC	AAG	TAC	AAG	CTA	GCT	CAC	ACG	GTT	CGA	ACG	CAT	ACC	GGA	911
Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Ala	His	Thr	Val	Arg	Thr	His	Thr	Gly	
		290				295						300				
GCT	GAC	GAC	AAG	TCT	TTT	GGA	TGT	GTG	CGG	CAA	GAA	GAA	GAT	GAT	AGC	959
Ala	Asp	Asp	Lys	Ser	Phe	Gly	Cys	Val	Arg	Gln	Glu	Glu	Asp	Asp	Ser	
	305					310					315					
GGT	AAA	ACC	GGA	GTT	AGT	TTG	TCA	AAA	GAC	ATA	ACC	GTT	GTT	GCC	GGG	1007
Gly	Lys	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Val	Val	Ala	Gly	
320					325					330					335	
ATA	ACG	GTT	CAG	AAA	AAC	ATA	ACA	ACA	TTG	GGT	CCG	TTG	GTT	CTT	CCT	1055
Ile	Thr	Val	Gln	Lys	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	
				340					345					350		
CTG	AGC	GAA	AAA	ATC	CTT	TTT	GTC	GTT	ACA	TTC	GTA	GCC	AAG	AAA	CTA	1103
Leu	Ser	Glu	Lys	Ile	Leu	Phe	Val	Val	Thr	Phe	Val	Ala	Lys	Lys	Leu	
			355				360						365			
TTA	AAA	GAT	AAG	ATC	AAA	CAC	TAT	TAC	GTG	CCG	GAT	TTC	AAA	CTT	GCA	1151
Leu	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	
		370					375					380				

GTA	GAT	CAT	TTC	TGT	ATT	CAT	GCG	GGA	GGT	AGA	GCC	GTG	ATA	GAT	GTG	1199
Val	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	
385						390					395					

TTA	GAG	AAG	AAC	TTA	GGG	CTA	TCG	CCG	ATA	GAT	GTG	GAG	GCA	TCA	AGA	1247
Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ser	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	
400					405					410					415	

TCA	ACA	TTA	CAT	AGA	TTT	GGG	AAT	ACA	TCG	TCT	AGT	TCA	ATT	TGG	TAT	1295
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	
				420					425					430		

GAA	TTA	GCA	TAC	ATA	GAG	CCA	AAA	GGA	AGG	ATG	AAG	AAA	GGT	AAT	AAA	1343
Glu	Leu	Ala	Tyr	Ile	Glu	Pro	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	
			435					440					445			

GCT	TGC	CAA	ATA	GCT	GGT	GGG	TCA	GGT	TTT	AAG	TGT	AAT	AGT	GCG	GTT	1391
Ala	Cys	Gln	Ile	Ala	Gly	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	
		450					455					460				

TGG	GTC	GCT	TTA	CGC	AAT	GTC	GAG	GCT	TCA	GCT	AAT	AGT	CCT	TGG	GAA	1439
Trp	Val	Ala	Leu	Arg	Asn	Val	Glu	Ala	Ser	Ala	Asn	Ser	Pro	Trp	Glu	
	465					470					475					

CAT	TGC	ATT	CAC	AAA	TAT	CCG	GTT	CAA	ATG	TAT	TCT	GGT	TCA	TCA	AAG	1487
His	Cys	Ile	His	Lys	Tyr	Pro	Val	Gln	Met	Tyr	Ser	Gly	Ser	Ser	Lys	
480					485				490						495	

TCA	GAG	ACT	CCT	GTC	CAA	AAC	GGT	CGG	TCC	TAATTTATGT	ATCTCAAATG	1537
Ser	Glu	Thr	Pro	Val	Gln	Asn	Gly	Arg	Ser			
				500								

ATGTTGTCCA	CTTTCTCTTT	TTTTTTTTTCT	TTTTTTTAGTT	ATAATTTAAT	GGTTACGATG	1597
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TTTTGTCTAG	GTCGTTATAA	ATAAAGAATA	CATGGGTGTT	ACTAGTATAA	AAAAAAAAAA	1657
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AAAAAAA	1664
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(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1732 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTTCTCTTCTT	CCCCAACA	ATG	ACC	CAT	AAC	CAA	AAC	CAA	CCT	CAC	CGG	GCA	51
		Met	Thr	His	Asn	Gln	Asn	Gln	Pro	His	Arg	Ala	
		1				5					10		
GTT CCG GTT CAC GTT ACA AAC TCC GAT CAA AAC CAA AAC CAA AAC CAA													99
Val Pro Val His Val Thr Asn Ser Asp Gln Asn Gln Asn Gln Asn Gln													
	15					20					25		
AAC AAT CTC CCA AAT TTT CTC TTA TCT GTT CGG CTC AAA TAT GTA AAA													147
Asn Asn Leu Pro Asn Phe Leu Leu Ser Val Arg Leu Lys Tyr Val Lys													
	30					35					40		
CTT GGG TAC CAT TAC CTA ATC TCC AAC GGT CTC TAC ATC CTC CTC CTC													195
Leu Gly Tyr His Tyr Leu Ile Ser Asn Gly Leu Tyr Ile Leu Leu Leu													
	45					50					55		
CCT CTC CTC GGC GGC ACA ATC GTA AAA CTC TCT TCC TTC ACA CTC AAC													243
Pro Leu Leu Gly Gly Thr Ile Val Lys Leu Ser Ser Phe Thr Leu Asn													
	60				65				70				75
GAA CTC TCT CTC CTC TAC AAC CAC CTC CGT TTT CAT TTC CTC TCC GCC													291
Glu Leu Ser Leu Leu Tyr Asn His Leu Arg Phe His Phe Leu Ser Ala													
	80							85					90
ACA CTC GCT ACC GGA CTC TTA ATC TCT CTC TCC ACC GCC TAC TTC ACC													339
Thr Leu Ala Thr Gly Leu Leu Ile Ser Leu Ser Thr Ala Tyr Phe Thr													
	95						100					105	
ACC CGT CCT CGT CAT GTC TTC CTC CTC GAC TTC TCA TGC TAC AAA CCT													387
Thr Arg Pro Arg His Val Phe Leu Leu Asp Phe Ser Cys Tyr Lys Pro													
	110					115					120		

GAC Asp	CCT Pro	TCC Ser	TTA Leu	ATA Ile	TGC Cys	ACT Thr	CGT Arg	GAA Glu	ACA Thr	TTC Phe	ATG Met	GAC Asp	CGA Arg	TCT Ser	CAA Gln	435
	125					130					135					
CGT Arg	GTA Val	GGT Gly	ATC Ile	TTC Phe	ACA Thr	GAA Glu	GAC Asp	AAC Asn	CTC Leu	GCT Ala	TTT Phe	CAA Gln	CAA Gln	AAG Lys	ATC Ile	483
140					145					150					155	
CTC Leu	GAA Glu	AGA Arg	TCC Ser	GGT Gly	CTT Leu	GGG Gly	CAG Gln	AAA Lys	ACT Thr	TAC Tyr	TTC Phe	CCT Pro	GAA Glu	GCT Ala	CTT Leu	531
				160					165						170	
CTT Leu	CGT Arg	GTT Val	CCT Pro	CCC Pro	AAT Asn	CCT Pro	TGT Cys	ATG Met	GAA Glu	GAA Glu	GCG Ala	AGA Arg	AAA Lys	GAA Glu	GCA Ala	579
			175					180						185		
GAG Glu	ACT Thr	GTT Val	ATG Met	TTC Phe	GGA Gly	GCT Ala	ATA Ile	GAC Asp	TCT Ser	GTT Val	CTT Leu	GAG Glu	AAA Lys	ACC Thr	GGT Gly	627
		190					195					200				
GTG Val	AAA Lys	CCT Pro	AAA Lys	GAT Asp	ATC Ile	GGA Gly	ATC Ile	CTT Leu	GTC Val	GTG Val	AAT Asn	TGT Cys	AGT Ser	TTG Leu	TTT Phe	675
	205					210					215					
AAT Asn	CCG Pro	ACG Thr	CCG Pro	TCA Ser	CTT Leu	TCC Ser	GCC Ala	ATG Met	ATT Ile	GTG Val	AAT Asn	AAG Lys	TAT Tyr	AAG Lys	CTT Leu	723
220					225					230					235	
AGA Arg	GGA Gly	AAC Asn	ATT Ile	TTG Leu	AGC Ser	TAT Tyr	AAT Asn	CTC Leu	GGT Gly	GGA Gly	ATG Met	GGT Gly	TGT Cys	AGT Ser	GCT Ala	771
				240					245					250		
GGA Gly	CTT Leu	ATC Ile	TCC Ser	ATT Ile	GAT Asp	CTC Leu	GCT Ala	AAA Lys	CAG Gln	CTT Leu	CTT Leu	CAG Gln	GTC Val	CAA Gln	CCA Pro	819
			255					260					265			
AAC Asn	TCA Ser	TAC Tyr	GCA Ala	CTA Leu	GTG Val	GTG Val	AGC Ser	ACA Thr	GAG Glu	AAC Asn	ATA Ile	ACC Thr	TTA Leu	AAC Asn	TGG Trp	867
		270					275					280				
TAC Tyr	TTA Leu	GGC Gly	AAC Asn	GAC Asp	CGA Arg	TCA Ser	ATG Met	CTT Leu	CTC Leu	TCT Ser	AAC Asn	TGC Cys	ATC Ile	TTC Phe	CGT Arg	915
	285					290					295					

ATG	GGA	GGA	GCC	GCC	GTA	CTT	CTC	TCA	AAC	CGT	TCC	TCC	GAT	CGC	ACC	963
Met	Gly	Gly	Ala	Ala	Val	Leu	Leu	Ser	Asn	Arg	Ser	Ser	Asp	Arg	Thr	
300					305					310					315	
CGT	TCA	AAA	TAT	CAG	CTC	ATC	CAC	CCC	GTC	CGT	ACC	CAC	AAA	GGA	GCC	1011
Arg	Ser	Lys	Tyr	Gln	Leu	Ile	His	Pro	Val	Arg	Thr	His	Lys	Gly	Ala	
				320					325					330		
AAC	GAC	AAC	GCA	TTT	GGC	TGC	GTT	TAC	CAA	CGA	GAA	GAC	AAC	AAC	GAA	1059
Asn	Asp	Asn	Ala	Phe	Gly	Cys	Val	Tyr	Gln	Arg	Glu	Asp	Asn	Asn	Glu	
			335					340					345			
GAA	GAA	ACC	GCC	AAA	ATC	GGA	GTC	TCA	CTC	TCT	AAA	AAC	CTA	ATG	GCA	1107
Glu	Glu	Thr	Ala	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asn	Leu	Met	Ala	
		350					355					360				
ATA	GCC	GGA	GAA	GCT	CTC	AAG	ACA	AAC	ATA	ACA	ACA	CTC	GGA	CCA	CTA	1155
Ile	Ala	Gly	Glu	Ala	Leu	Lys	Thr	Asn	Ile	Thr		Leu	Gly	Pro	Leu	
	365					370					375					
GTC	TTA	CCA	ATG	TCC	GAA	CAG	ATT	CTG	TTT	TTC	CCA	ACA	CTC	GTG	GCT	1203
Val	Leu	Pro	Met	Ser	Glu	Gln	Ile	Leu	Phe	Phe	Pro	Thr	Leu	Val	Ala	
380					385					390					395	
CGA	AAA	ATC	TTC	AAA	GTC	AAG	AAA	ATA	AAG	CCT	TAC	ATA	CCC	GAT	TTC	1251
Arg	Lys	Ile	Phe	Lys	Val	Lys	Lys	Ile	Lys	Pro	Tyr	Ile	Pro	Asp	Phe	
				400					405					410		
AAG	CTA	GCT	TTC	GAG	CAT	TTC	TGC	ATC	CAT	GCG	GGA	GGT	AGA	GCA	GTG	1299
Lys	Leu	Ala	Phe	Glu	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	
			415					420					425			
CTT	GAT	GAG	ATA	GAG	AAG	AAT	TTG	GAT	TTA	TCA	GAG	TGG	CAT	ATG	GAA	1347
Leu	Asp	Glu	Ile	Glu	Lys	Asn	Leu	Asp	Leu	Ser	Glu	Trp	His	Met	Glu	
		430					435					440				
CCA	TCG	AGG	ATG	ACT	TTA	AAC	CGG	TTT	GGT	AAT	ACT	TCG	AGT	AGC	TCA	1395
Pro	Ser	Arg	Met	Thr	Leu	Asn	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	
	445					450					455					
CTT	TGG	TAT	GAA	CTT	GCG	TAT	AGT	GAA	GCT	AAA	GGG	AGG	ATT	AAG	AGA	1443
Leu	Trp	Tyr	Glu	Leu	Ala	Tyr	Ser	Glu	Ala	Lys	Gly	Arg	Ile	Lys	Arg	
460					465					470					475	

GGA GAT AGG ACT TGC CAA ATT GCG TTT GGA TCG GGA TTT AAG TGT AAT	1491
Gly Asp Arg Thr Cys Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn	
480 485 490	
AGT GCG GTT TGG AAA GCT TTG AGA ACC ATT GAT CCT ATT GAT GAG AAG	1539
Ser Ala Val Trp Lys Ala Leu Arg Thr Ile Asp Pro Ile Asp Glu Lys	
495 500 505	
AAG AAT CCA TGG AGT GAT GAG ATT CAT GAG TTT CCA GTT TCT GTT CCT	1587
Lys Asn Pro Trp Ser Asp Glu Ile His Glu Phe Pro Val Ser Val Pro	
510 515 520	
AGG ATC ACT CCA GTT ACT TCT AAC TAGTGTTTTT TTTTGGGTC CAACTAGGGA	1641
Arg Ile Thr Pro Val Thr Ser Asn	
525 530	
TAATATTTGT TATGGTTTTG TTCTTACGTA CGTACTTTAA GTGATTTAGT CTAAAAATAA	1701
ATTGGTTTCA TAAAAA AAAA A	1732

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27 :

AAG CTT AAA CTA GTA TAC CAT TAC TTG ATC TCC AAC GCC ATG TAT TTG	48
Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Met Tyr Leu	
1 5 10 15	
TTA ATG GTG CCG CTT CTA GCA GTA GCC TTT GCT CAT CTC TCC ACG TTG	96
Leu Met Val Pro Leu Leu Ala Val Ala Phe Ala His Leu Ser Thr Leu	
20 25 30	

ACG	ATT	CAA	GAT	CTG	GTT	CAT	CTT	TGG	GAA	CAG	CTT	AAG	TTC	AAT	TTA	144
Thr	Ile	Gln	Asp	Leu	Val	His	Leu	Trp	Glu	Gln	Leu	Lys	Phe	Asn	Leu	
		35					40					45				
CTG	TCA	GTA	ACT	CTC	TGC	TCG	AGC	CTT	ATG	GTG	TTT	TTA	GGG	ACT	CTG	192
Leu	Ser	Val	Thr	Leu	Cys	Ser	Ser	Leu	Met	Val	Phe	Leu	Gly	Thr	Leu	
	50					55					60					
TAT	TTC	ATG	AGC	CGA	CCG	ACG	AAG	ATT	TAC	TTG	GTG	GAT	TTC	TCT	TGT	240
Tyr	Phe	Met	Ser	Arg	Pro	Thr	Lys	Ile	Tyr	Leu	Val	Asp	Phe	Ser	Cys	
65					70					75					80	
TAC	AAG	CCG	GAA	AAA	GAG	CGT	ATA	TGC	ACG	AGA	GAG	ATT	TTC	TAT	GAG	288
Tyr	Lys	Pro	Glu	Lys	Glu	Arg	Ile	Cys	Thr	Arg	Glu	Ile	Phe	Tyr	Glu	
				85				90						95		
AGA	TCG	AAA	CTA	ACT	GGG	AAT	TTT	ACC	GAT	GAT	AAT	TTA	ACT	TTC	CAA	336
Arg	Ser	Lys	Leu	Thr	Gly	Asn	Phe	Thr	Asp	Asp	Asn	Leu	Thr	Phe	Gln	
			100					105					110			
AAG	AAA	ATT	ATC	GAA	AGA	TCT	GGA	TTA	GGT	CAG	AAC	ACG	TAC	TTA	CCT	384
Lys	Lys	Ile	Ile	Glu	Arg	Ser	Gly	Leu	Gly	Gln	Asn	Thr	Tyr	Leu	Pro	
		115					120					125				
GAG	GCC	GTT	CTA	CGG	GTT	CCG	CCC	AAT	CCG	TGT	ATG	GCG	GAG	GCT	AGA	432
Glu	Ala	Val	Leu	Arg	Val	Pro	Pro	Asn	Pro	Cys	Met	Ala	Glu	Ala	Arg	
	130					135					140					
AAG	GAG	GCT	GAG	ATG	GTT	ATG	TTC	GGT	GCG	ATC	GAT	GAA	TTG	TTG	GAG	480
Lys	Glu	Ala	Glu	Met	Val	Met	Phe	Gly	Ala	Ile	Asp	Glu	Leu	Leu	Glu	
145				150					155						160	
AAA	ACC	GGG	GTT	AAA	CCT	AAG	GAT	ATC	GGT	ATT	CTT	GTG	GTG	AAT	TGC	528
Lys	Thr	Gly	Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	
				165				170						175		
AGC	TTG	TTC	AAT	CCG	ACG	CCG	TCT	CTG	TCC	GCA	ATG	GTG	GTT	AAT	CGG	576
Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Arg	
			180					185					190			
TAC	AAG	CTT	AGA	GGG	AAT	ATC	ATA	AGT	TAT	AAC	CTT	GGC	GGG	ATG	G	622
Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Ile	Ser	Tyr	Asn	Leu	Gly	Gly	Met		
		195				200						205				

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28 :

Asn Ile Thr Thr Leu Gly
5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29 :

Ser Asn Cys Lys Phe Gly
5

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAUCAUCAUC AUGTCGACAA AATGACGTCC ATTAACGTAA AG

42

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31 :

CUACUACUAC UAGTCGACGG ATCCTATTTG GAAGCTTTGA CATTGTTTAG

50

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE: Xaa at position 3 = Leu or Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32 :

Lys Leu Xaa Tyr His Tyr
5

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33 :

CAUCAUCAUC AUGAATTCAA GCTTAARYTN BKNTAYCAYT A

41

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34 :

Asn Leu Gly Gly Met Gly Cys
5

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35 :

CAUCAUCAUC AUGAATTCAA GCTTAAYYTN GGNGGNATGG G

41

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36 :

CUACUACUAC UAGGATCCGT CGACCCATNC CNCCNARRTT

40

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37 :

Gly Phe Lys Cys Asn Ser

5

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other
 (A) DESCRIPTION: synthetic oligonucleotide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38 :
 CUACUACUAC UAGGATCCGT CGACSWRTTR CAYTTTRAANC C

41

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other
 (A) DESCRIPTION: synthetic oligonucleotide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39 :
 CUACUACUAC UASWRTTRCA YTTRAANCC

29